

- Puchkov YuM, et al. 1996. The academician P.P. Luk'yanenko and breeding of winterhardy winter wheat cultivars. Krasnodar Agricultural Research Institute Work. Pp. 71-86 (In Russian).
- Puchkov YuM, Bespalova LA, Kolesnikov FA, et al. 2001. VIR world collection catalogue. N733. Cultivars and breeding lines of winter bread and durum wheat, winter triticale of Krasnodar Research Institute (In Russian).
- Stuchlova E and Kovacikova E. 1993. Wheat breeding against fusarioses. Genet. a Slecht **29** (2):139-160.
- Terekhina NA. 1993. Sources of resistance to scab of wheat. Breeding and Seed Frowing 5-6:23-24 (In Russian).items from the republic of south africa

## **ARC-SMALL GRAIN INSTITUTE**

**Private Bag X29, Bethlehem 9700, South Africa**

**<http://www.arc-sgi.agric.za>**

### ***Preharvest sprouting, falling number, and extreme temperature research.***

M. Craven.

The main aim of the preharvest-sprouting program is the routine evaluation of wheat cultivars for their preharvest sprouting susceptibility. Wheat breeding material from the Small Grain Institute's Plant Breeding Division also is screened for PHS resistance to ensure that cultivars released within the program has the required PHS resistance. Aside from this routine screening, the possibility was investigated that cultivars might show a different PHS score when the cultivars are subjected to various fertilizer levels.

Because PHS is closely associated with falling number (FN), an intensive research program was maintained for the past few years that investigated FN and cultivar response regarding FN to various external factors. The factors investigated focused on the implementation of an FN-management system within a general wheat-production practice. The effect of kernel moisture content, fertilizer application, and glyphosate treatments to enhance the drying period of wheat and reduce the occurrence of green kernels are projects that were finalized during the 2004–05 season at Small Grain Institute. Because FN is an important quality factor evaluated within the wheat grading regulations, the possibility of managing FN within various wheat production practices would add enormously to the wheat industry.

In April 2004, an extreme temperature trial was initiated in collaboration with the University of the Free State. The effect of extreme high (35°C) and low (–4°C) temperatures during various grain-filling stages on specified quality parameters on selected cultivars will be investigated over a 2-year period. Some of the quality parameters investigated include FN, protein composition, starch damage, yield, and hectoliter mass. All temperature simulations are based on actual temperatures recorded over approximately 6 years. We hope that this research will shed light on cultivars that might respond better to such extreme 'freak' temperature occurrences. The data generated could be used either in breeding programmes or serve as guidelines on general production practices in risk areas that might be prone to such extreme temperature occurrences.

### ***Wheat production in South Africa.***

A. Barnard, W.M. Otto, and T. Walsh.

There are three dominant production systems in South Africa, under dryland conditions in both summer and winter rainfall regions and under irrigation conditions on a country wide basis. Almost 50 % of the South African wheat production is accounted for by cultivation under dryland conditions in the Summer Rainfall Region, whereas wheat production in the Winter Rainfall Region and under irrigation accounts for the remaining production in South Africa. A national cultivar evaluation program is conducted each year at Small Grain Institute that entails the evaluation and characterization of all newly classified and released wheat cultivars of all seed companies on an objective and scientific basis.

The objectives of this program are mainly to characterize cultivars in terms of yield performance and yield stability, hectoliter mass, falling number, and protein content, and other grain quality parameters, over environments and years. Another major objective is to compare cultivars in terms of agronomic characteristics, such as growth period, straw strength, shattering, and yield components and to make reliable and scientifically sound recommendations to producers and other role-players for all production regions of South Africa.

The results of the program enable producers, including small-scale farmers, to make well-informed production decisions in terms of cultivar choice. Cultivar choice is a critical production decision that will greatly affect the profitability of the producer's enterprise.

### ***Summer Rainfall Region.***

**Dryland production.** Almost half of the South African wheat production is accounted for by cultivation under dryland conditions in the Summer Rainfall Region. Because of the large variation in climatic conditions and soil types existing in this region, wheat production is very challenging. Not only are good cultivation and management practices essential for successful wheat production, but also the correct cultivar choice. The dryland production area is divided mainly into four homogenous areas where different cultivars, mainly winter and intermediate types, are planted. Cultivar evaluation trials were planted at 17 sites throughout the Western, Central, and Eastern Free State, and parts of Mpumalanga. The trials were successfully carried out and were reported. Twenty entries were included in the trials, of which eight were from Small Grain Institute, five from Monsanto, and seven from PANNAR.

**Production under irrigation.** Wheat produced under irrigation amounts to about 20 % of the total wheat production of South Africa, and has a stabilizing influence on the total production. There are currently six major irrigation regions, although irrigation farming is expanding into new production regions.

Mainly spring wheat cultivars are planted in a total of 60 evaluation trials at 31 localities in the different irrigation areas. Entries in these trials originated from Small Grain Institute (6) and from Monsanto (6). Two advanced breeding lines also were included. Analyses of variance, AMMI analysis, and biplots are used in the interpretation of results, and identifying cultivar adaptation and stability in the different production regions. Results from these trials are available in a detailed report.

### ***Winter Rainfall Region.***

There are mainly two wheat producing areas in the Winter Rainfall Region:

- *The Swartland area* stretches from Durbanville in the south to the Sandveld area around Elandsbaai in the north and from Saldana Bay in the west to the mountain ranges in the east.
- *The Rûens or South Coast area*, stretches from Botrivier in the west to the Albertina-district in the east and from Aghullas in the south to the Langeberg mountain range north of Greyton through to Riversdal.

The Winter Rainfall Region is well suited to the production of spring wheats, which do not require the same amount of cold to break their dormancy, as that of the winter wheat cultivars grown in the rest of South Africa. Cultivar choice in the Winter Rainfall Region is of extreme importance due to the varied climatic differences between cultivation areas. The cultivars available differ in their yield reaction to the changing yield potential conditions that exist in the Winter Rainfall Region. Other important factors which have also to be taken into consideration are grain quality, hectoliter mass and disease susceptibility.

The Cultivar Evaluation Program in the Winter Rainfall Region is run jointly by the Small Grain Institute and The Directorate of Agriculture of the Western Cape. The program consists of 13 sites in the Swartland and 14 sites in the Rûens, with 14 cultivars included in the trials. The cultivars, from ARC-Small Grain Institute, Monsanto, and PANNAR, are tested annually for yield potential, quality, disease resistance, and adaptability.

---

***Verification of cultivars suitable for production in resource limited agriculture.***

S. Ramburan.

As part of the National Cultivar Evaluation Programme the Small Grain Institute has introduced a related programme in 2003 that involves the screening of wheat cultivars suitable for production in resource limited agriculture. The differences in production practices and resources of small-scale enterprises in comparison to commercial situations necessitated the introduction of cultivar evaluation work in the resource limited areas of the country. A large proportion of resource limited farmers in the major wheat producing regions of South Africa have the potential for commercialization and correct cultivar choice is sure to assist them in reaching this ultimate goal.

Cultivar evaluation trials were planted at various small-scale farms which were representative of specific wheat producing regions in 2004. A total of five dryland trials (20 cultivars) and four irrigation trials (15 cultivars) were planted. Cultivars originated from three different institutes, Small Grain Institute, Pannar, and Monsanto. During the season the adaptability of the cultivars to the production environments were evaluated through observations of emergence problems, growth period and disease damage. Statistical analyses were utilized to determine the yield and quality performance of the cultivars in the different environments.

The data obtained from the project will be used to ultimately characterize the different cultivars in terms of their suitability for production in different resource limited areas. These results, together with those expected in 2005 and 2006 will eventually be used to assist small-scale wheat producers with reliable recommendations that are based on applicable scientific research.

***Small Grain Institute Laboratories: Seed Testing Laboratory.***

H. Hatting.

Seed plays a vital role in the potential crop yield of each small grain producer. Small grain seed must comply with legal requirements with regard to the purity and germination percentage before it can be marketed. The Small Grain Institute has a registered Seed Testing Laboratory in which international methodology [viz. ISTA (International Seed Testing Association) methods] is used to determine the quality characteristics of seed. The germination and purity testing over the past year resulted in 474 analyses, in which the quality of each seed lot was tested to ensure that poor quality seed would not be planted. The laboratory provides a unique service. Having the infrastructure and experience, seed analyses are conducted objectively on a commercial and need driven basis for the seed industry.

The laboratory was visited by several schools. This work contributes favorably to the income of the Seed Testing Laboratory. The services are client specific and extended the commercial services of the laboratory.

***Small Grain Institute Laboratories: Wheat Quality Laboratory.***

C.W. Miles.

The Wheat Quality Laboratory plays an integral part in the breeding process and accurate and reliable data for researchers must be ensured. To accomplish accuracy and reliability, the laboratory takes part in ring tests sent out by Sasko, monthly, and the South African Grain Laboratory, quarterly.

During the past year, a total of 70,033 analyses were performed for researchers at Small Grain Institute and 5,373 analyses were performed for external clients such as Omnia Fertilizer, PANNAR, and SENWES Co-operation.

***Personnel.***

Klaus Pakendorf joined Small Grain Institute as a wheat breeder in Stellenbosch, and Solomon Fekybelu, a researcher handling the irrigation program, at Plant Breeding in Bethlehem. Tholi Mazibuko was appointed as a researcher at Crop

Science and manages the falling number and preharvest-sprouting programs. Eric Morojele was appointed as a researcher at Soil Management. Brian de Villiers from Plant Protection resigned and was replaced by Hestia de Wet. Lucas Serage also resigned from the Soil Management section.

### ***Publications.***

- Barnard A. 2004 . Comparing different methods in estimating sprout damage in wheat. **In:** SASPC Congress, 20-22 January 2004, Bloemfontein, South Africa.
- Hatting JL, Wraight SP, and Miller RM. 2004. Efficacy of *Beauveria bassiana* (Hyphomycetes) for control of Russian wheat aphid (Homoptera: Aphididae) on resistant wheat under field conditions. *Biocontrol Sci Tech* 14(5):459-473.
- Labuschagne MT, and Aucamp JC. 2004. The use of size exclusion high performance liquid chromatography (SE-HPLC) for wheat quality prediction in South Africa. *South Afr J Plant Soil* 21(1):8-12.
- Maeko TC. 2004 . Irrigation management eight wetting front detectors. **In:** SASPC Congress, 20-22 January 2004, Bloemfontein, South Africa.
- Ntushelo K and Crous PW. 2004. Fungicide sensitivity in *Tapesia yallundae* populations collected from 15 wheat fields in the Western Cape province of South Africa. *South Afr J Plant Soil* 21(2):104-108.
- Ramburan VP, Prins R, Pretorius ZA, Boyd LA, Smith PH, Louw JH, and Boshoff WHP. 2004. A genetic analysis of adult plant resistance to stripe rust in the wheat cultivar Kariëga. *Theor Appl Genet* 108(7):1426-1433.
- Tolmay JPC. 2004. The effect of different crop residues, tillage systems and nitrogen applications on the yield of wheat within a crop rotation system in the Eastern Free State. **In:** SASPC Congress, 20-22 January 2004, Bloemfontein, South Africa.
- Tolmay VL. 2004. Yield evaluation of Russian wheat aphid resistant cultivars in the Eastern Free State. **In:** SASPC Congress, 20-22 January 2004, Bloemfontein, South Africa.
- Tolmay VL, Prinsloo GJ, Maré R, and Hatting JL. 2004. Resistant cultivars for Russian wheat aphid control: the South African experience. **In:** Proc 16th Biennial Internat Plant Resistance to Insect Workshop, 21-23 March 2004, Baton Rouge, Louisiana, USA.
- Tolmay VL and Tjallingi WF. 2004. DC Electronic monitoring of Russian Wheat Aphid feeding behaviour on susceptible and resistant wheat. **In:** Proc 16th Biennial Internat Plant Resistance to Insect Workshop, 21-23 March 2004, Baton Rouge, Louisiana, USA.
- Tolmay VL and Van Deventer CS. 2004. Field evaluation of Russian wheat aphid resistant cultivars in South Africa. **In:** Proc 16th Biennial Internat Plant Resistance to Insect Workshop, 21-23 March 2004, Baton Rouge, Louisiana, USA.

## **UNIVERSITY OF STELLENBOSCH**

**Department of Genetics, Private Bag X1, Matieland 7602, South Africa.**

G.F. Marais, H.S. Roux, A.S. Marais, W.C. Botes, K.W. Pakendorf, and J.E. Snyman.

### ***Triticale breeding.***

Our breeding program continued and promising new lines were selected. The 2004 growing season was abnormally dry and in the elite trials the six commercial triticale cultivars, USGEN 19, Rex, Kiewiet, Bacchus, Tobie, and Ibis, on average, outyielded the leading wheat cultivars by about 20 %. Of the released cultivars, Tobie had the best yield and hectoliter mass.

### ***Wheat recurrent mass selection.***

A large-scale, recurrent mass selection program based on hydroponic culture of cut male sterile (*Ms3ms3*) tillers was continued. In the summer of 2004–05, some 500 F<sub>4</sub> inbred lines (2003 crosses) and 1,800 F<sub>6</sub> inbreds (2002 crosses) were developed using field planting and single-seed descent in the off-season. Approximately 60,000 new F<sub>1</sub> were produced. The program is continuously being refined and strong selection pressure is maintained for mildew, rust and Septoria

resistance. In 2004, we began to experiment with MAS of four gene complexes, i.e., the *Ae. ventricosa*-derived *Lr37/Sr38/Yr17* cluster, the *S. cereale*-derived *Sr31/Lr26/Pm8/Yr9* cluster (without *Sec1* locus), the *Th. ponticum*-derived *Lr19* gene (without yellow pigment locus), and the *Sr24/Lr24* complex (*Th. elongatum*). Currently, published marker systems for the *Lr21*, *Lr34/Yr18* and *Sr2* genes are being evaluated for their utility in recurrent selection. In 2005, we will implement routine MAS directed at the *Lr37* complex, which will supplement rather than replace conventional seedling and field resistance screening and will be kept up for 2–3 seasons when the frequency of the gene complex in the base population should have reached a level of 0.70–0.80. At this point, a new gene(s) will be targeted for MAS.

### **Genetic studies.**

In our program aimed at the transfer of rust resistance genes from wild relatives, linked leaf rust (*Lr53*) and stripe rust (*Yr35*) resistance genes introgressed from *T. turgidum* subsp. *dicoccoides* were found to be located on chromosome arm 6BS of the cross derivative, 98M71. We also translocated (centric break and fusion) linked leaf rust (*Lr54*) and stripe rust (*Yr37*) resistance genes from *Ae. kotschyi* to wheat chromosome arm 2DL. The latter resistance genes appear to be associated with an *Rht*-gene as well as a gene affecting daylight sensitivity. Attempts to determine the chromosome location of genes that were introgressed from *Ae. sharonensis* and *Ae. peregrina* were continued. Experiments were initiated to disrupt meiotic chromosome pairing through *Ph1b* deficiency in hybrids carrying disease resistance genes on translocation/ addition chromosomes from *Ae. speltoides*, *Ae. biuncialis*, and *Ae. caudata*. Test cross derivatives from these material are being screened for useful recombinants. A recombined *Lr19* translocation, *Lr19-149-299*, was used in an attempt to shorten it still further through use of *ph1b*-induced homoeologous pairing. Testcross progeny, which may have lost the segregation distortion gene, *Sd2*, are being characterized in segregation and GISH analyses.

A program aimed at transferring salt tolerance from *Th. distichum* to triticale was continued. Backcrosses to develop disomic additions for the remaining three of five target chromosomes were made, as were attempts to find PCR-based markers for each critical chromosome.

### **Publications.**

- Snyman JE, Pretorius ZA, Kloppers FJ, and Marais GF. 2004. Detection of adult-plant resistance to *Puccinia triticina* in a collection of wild *Triticum* species. *Genet Res Crop Evol* 51:591-597.
- Jacobs JA, Hanekom L, Marais AS, and Marais GF. 2004. Development of SCAR markers for a *Thinopyrum distichum* chromosome that appears to be involved in salt tolerance. *SAJ Plant Soil* 21:236-239.

---

ITEMS FROM SPAIN**UNIVERSIDAD POLITÉCNICA DE MADRID**

**Departamento de Biotecnología, E.T.S.I. Agrónomos, C. Universitaria, 28040, Madrid, Spain.**

A. Delibes, I. López-Braña, S. Moreno-Vázquez, and C.M. González-Belinchón.

**CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS**

**Departamento de Protección Vegetal, Centro de Ciencias Medioambientales, Serrano, 115, 28006, Madrid, Spain.**

M.D. Romero and M.F. Andrés.

**UNIVERSIDAD DE LLEIDA**

**Departamento de Producción Vegetal y Ciencia Forestal, Institut de Recerca i Tecnologia Agroalimentaries (UdL-IRTA), Lleida, Spain.**

J.A. Martín-Sánchez, G. Briceño-Félix, E. Sin, C. Martínez, and A. Michelena.

**CONSEJERÍA DE INFRAESTRUCTURAS Y DESARROLLO TECNOLÓGICO**

**Servicio de Investigación y Desarrollo Tecnológico (SIDT), Ap. 22, CP 06080, Badajoz, Spain.**

J. Del Moral de la Vega, Fco. Pérez Rojas, and M. Senero Fernández.

***Resistance of advanced bread wheat lines to nematodes and Hessian fly—progress update.***

**Resistance to *H. avenae*.** *Heterodera avenae*-resistance gene *Cre2*, transferred from *Aegilops ventricosa* AP-1, has been introduced to advanced bread wheat lines with suitable agronomic traits of interest (quality and/or production) via backcrossing. The resistance gene *Cre2* has shown to confer a high level of resistance to the Spanish pathotype Ha71 (Montes et al. 2003). The hexaploid H-93-derived lines from the cross '*T. turgidum* subsp. *turgidum* cv. Rubroastrum, H-1-1/*Ae. ventricosa* AP-1//*T. aestivum* subsp. *aestivum* cv. Almatense, H-10-15' previously described by Delibes et al. (1993), hereafter the selected line H-93-8, was employed as a donors in a hexaploid wheat background. Different commercial wheat cultivars such as Anza, Rinconada, Cajeme, Cartaya, Betres, Marius, and Osona were used as recurrent parents. All crosses were carried out in a greenhouse using standard manual procedures, obtaining two generations/year. Following successive backcrossing (BC<sub>4</sub>) and selfing, the resulting desirable lines were evaluated for favorable agronomic traits and cereal cyst nematode (CCN) resistance under field conditions in four locations in Spain (Toledo, La Poveda, Giménez, and Foradada).

Thus, selected lines were consistently tested for CCN resistance, yield and other agronomic traits from 1999 through 2002. Based on 2 years of data at several locations, the cross 'H-93-8/4\*Rinconada', under the designation ID-2150, was found to exhibited excellent agronomic characteristics, grain yield, and adequate resistance to CCN under growers conditions (Fig 1). In the autumn of 2003, the line ID-2150 was advanced to be evaluated in the national cultivar testing and registration yield trial at the Spanish Office of Vegetable Variety (OEVV).

**Resistance to *M. destructor*.** *Mayetiola destructor*-resistance gene *H27*, transferred from *Ae. ventricosa*, has been introduced to advanced bread wheat lines with suitable agronomic traits of interest via backcrossing. The resistance gene

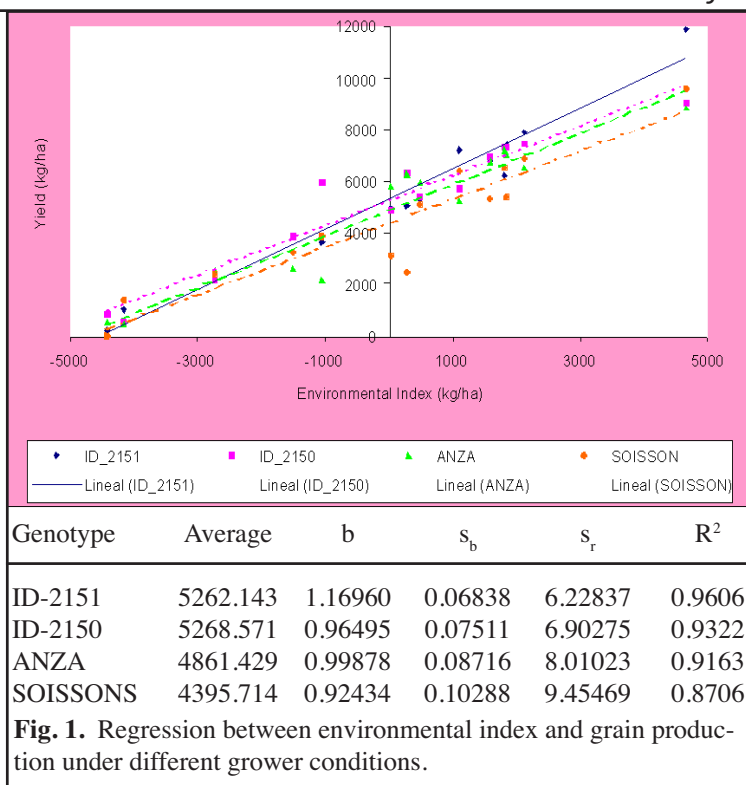
H27 has shown to confer resistance to *M. destructor* to the Spanish biotype (Martín-Sánchez et al. 2003). The 4D/4M<sup>v</sup> wheat/*Aegilops ventricosa* substitution line H-93-33, from the cross '*T. turgidum* subsp. *turgidum* cultivar Rubroatrum, H-1-1/*Ae. ventricosa* AP-1//*T. aestivum* subsp. *aestivum* cultivar Almatense, H-10-15' previously described by Mena et al. (1989, 1993) and Delibes et al. (1993), hereafter H-93-33/H-10-15, were employed as a donors in a hexaploid wheat background. Different commercial wheat varieties such as Anza, Rinconada, Cajeme, Cartaya, Betres, Marius, Adalid, Astral, Recital, Alcotan, and Osona were used as recurrent parents. All crosses were carried out in a greenhouse using standard manual procedures, obtaining two generations/year. Following successive backcrossing (BC<sub>4</sub> and BC<sub>5</sub>) and selfing, the resulting lines were evaluated for favorable agronomic traits and Hessian fly resistance under field conditions in Azuaga (Badajoz) Spain.

Thus, selected lines were consistently tested for Hessian fly resistance, yield and other agronomic traits from 2000 through 2003. Based on 2 years of data at several locations, the cross H-93-33 / H-10-15 / 5\* ADALID, under the designation ID-2151 was found to exhibited excellent agronomic characteristics, yield grain and moderate resistance to Hessian fly under growers conditions (Fig. 1). In the autumn of 2003, the line ID-2151 was advance to be evaluated in the national cultivar testing and registration yield trial at the Spanish Office of Vegetable Variety (OEVV).

**Financial support.** This work was supported by grants AGL2001-3824-C04 and 2004-06791-CO4 from the Comisión Interministerial de Ciencia y Tecnología of Spain.

## References.

- Delibes A, Romero MD, Aguaded S, Duce A, Mena M, López-Braña I, and Andrés MF. 1993. Resistance to the cereal cyst nematode (*Heterodera avenae*) transferred from the wild grass *Aegilops ventricosa* to hexaploid wheat by a "stepping stone" procedure. *Theor Appl Genet* 87:402-408.
- Martín-Sánchez JA, Gómez-Colmenarejo M, Del Moral J, Sin E, Montes MJ, González-Belinchón C, López-Braña I, and Delibes A. 2003. A new Hessian fly resistance gene resistant to the cereal cyst nematode (*Heterodera avenae*) transferred from the wild grass *Aegilops ventricosa* to hexaploid wheat by a "stepping stone" procedure. *Theor Appl Genet* 87:402-408.
- Mena M, Orellana J, López-Braña I, García-Olmedo F, and Delibes A. 1989. Biochemical and cytological characterization of wheat/*Aegilops ventricosa* addition and transfer lines carrying chromosome 4M<sup>v</sup>. *Theor Appl Genet* 77:184-188.
- Mena M, Orellana J, López-Braña I, García-Olmedo F, and Delibes A. 1993. Characterization of wheat/*Aegilops ventricosa* introgression and addition lines with respect to the M<sup>v</sup> genome. *Theor Appl Genet* 86:197-204.
- Montes MJ, López-Braña I, Romero MD, Sin E, Andrés MF, Martín-Sánchez JA, and Delibes A. 2003. Biochemical and genetic studies of two *Heterodera avenae* resistance genes transferred from *Aegilops ventricosa* to wheat. *Theor Appl Genet* 107:611-618.



**Personnel.**

Guillermo Briceño-Félix has joined the Institut de Recerca I Tecnologia Agroalimentaries (Centre UdL-IRTA) as a cereal breeder on April 2004.

**Publications.**

- Delibes A, López-Braña I, Montes MJ, Gómez-Colmenarejo M, González-Belinchón C, Romero D, Andrés MF, Martín-Sánchez JA, Sin E, Martínéz C, and Michelena A. 2002. Differential induction of defence-enzymes and chromosomal location of two *Heterodera avenae* resistance genes transferred to wheat from *Aegilops ventricosa*. Ann Wheat Newslet 48:165-167.
- Delibes A., López-Braña I, Montes MJ, González-Belinchón C, Martín-Sánchez JA, Sin E, Martínéz C, Michelena A, del Moral J, Perez-Rojas F, and Espinal FJ. 2002. Resistance to Hessian fly conferred by the gene *H27*. Relationships with other sources of resistance and its effect in some agronomic traits. Ann Wheat Newslet 48:165-167.
- Delibes A, López-Braña I, Moreno-Vázquez S, González-Belinchón CM, Romero MD, Andrés MF, Martín-Sánchez JA, Sin E, Martínéz C, and Michelena A. 2002. Changes in preoxidase gene expresión in response to *Heterodera avenae* infection in a wheat/*Aegilops ventricosa* introgression line carrying the resistance gene *Cre2*. Ann Wheat Newslet 48:165-167.
- Delibes A., López-Braña I, Montes MJ, González-Belinchón C, Martín-Sánchez JA, Sin E, Martínéz C, Michelena A, del Moral J, Perez-Rojas F, Espinal FJ, and Senero M. 2003. Studies in relation to the Hessian fly resistance gene (*H30*) transferred from the wild grass *Aegilops triuncialis* to hexaploid wheat. Ann Wheat Newslet 49:142-144.
- Del Moral J, Delibes A, Martín-Sánchez JA, Mejias A, López-Braña I, Sin E, Montes MJ, Perez-Rojas F, Espinal F, and Senero M. 2002. Obtención de líneas de trigo resistentes a *Mayetiola destructor* Say en la campiña sur de Extremadura. Boletín Sanidad Vegetal 28 (4):585-590.
- Montes MJ, Martín Sánchez JA, González-Belinchón CM, López-Braña I, Delibes A, Sin E, and Martinez C. 2003. Characterisation by isozyme analysis of a wheat/*Aegilops triuncialis* introgression line carrying resistance to Cereal Cyst Nematode and Hessian fly. **In:** Biotic and Abiotic Stresses (Pogna N, et al. Eds). SIMMI, Roma, Italy. Pp. 1211-1213.
- Montes MJ, López-Braña I, and Delibes A. 2004. Root enzyme activities associated with resistance to *Heterodera avenae* conferred by gene *Cre7* in a wheat/*Aegilops triuncialis* introgression line. J Plant Physiol 161:493-495.
- Montes MJ, Benavente E, López-Braña I, and Delibes A. 2004. Biochemical and cytological characterisation of a wheat/*Aegilops triuncialis* introgression line carrying resistance to cereal cyst nematode and Hessian fly. Theor Apple Genet (submitted).
- Martín-Sánchez JA, Montes MJ, López-Braña I, Romero MD, Sin E, Martínéz C, Andrés MF, Gómez-Colmenarejo M, González-Belinchón C, and Delibes A. 2003. Differential induction of defence-enzymes and chromosomal location in wheat/*Aegilops ventricosa* introgression lines of *Cre2* and *Cre5 heterodera avenae* resistance genes. A progress report. **In:** Breeding strategies for Small Grains Cereals in the Third Millennium, EUCARPIA (Marè C, Faccioli P, and Stanca AM, Eds). Pp. 307-309.

**ITEMS FROM SWEDEN**

**THE NORDIC GENE BANK**  
**P.O. Box 41, SE230 53, Alnarp, Sweden.**

***Triticum accessions in the collections of the Nordic Gene Bank.***

Fredrik Ottosson, Louise Bondo, Oscar Diaz, and Bent Skovmand.

The Nordic Gene Bank (NGB) is a centre for conservation, documentation, and utilization of plant genetic resources within the Nordic region. The NGB was founded in 1979 and is an institute under the Nordic Council of Ministers. The

mandate of NGB is to conserve cultivated species and their wild relatives within the region that involves the countries of Denmark, Finland, Island, Norway, and Sweden, and the three independent areas of Greenland, Faeroe Islands, and Aaland.

The conservation strategy is based on simple and cost-effective techniques, utilizing freezers for seed storage. The seed material is maintained in a central seed storage facility and divided into three separate collections. The active collection is for distribution, characterization, and multiplication. The base collection is for long-term conservation, and the safety duplication collection is a replicate of the base collection and is stored on Svalbard.

The NGB information and documentation system contains extensive information about the mandate species and the material stored. The material is easily accessible to users at <http://www.ngb.se>. The NGB promotes strategic and applied research projects on the mandate species to improve conservation and utilization of its genetic resources. The genetic resources in the NGB collections are managed according to the Kalmar agreement (Access and Rights to Genetic Resources: A Nordic Approach. 2003. Nord 2003:16, Nordic Council of Ministers, Copenhagen), which states that NGB genetic resources are managed in the public domain and freely available to bona fide users.

### ***Triticum at the Nordic Gene Bank.***

In the collections at the NGB, there are 1,543 accessions of *Triticum* sp. (Table 1). Close relatives, such as *Aegilops* and *Secale*, also are represented in the collections. The majority of the above listed accessions belong to the “ordinary collection” of the NGB. In addition, the gene bank maintains several subcollections in which accessions of *Triticum* and close relatives can be found:

**Table 1** . Accessions of *Triticum* and close relatives maintained by the Nordic Gene Bank, Alnarp, Sweden.

No. of accessions	Species	No. of accessions	Species
1,199	<i>T. aestivum</i> subsp. <i>aestivum</i>	11	<i>T. timopheevii</i>
11	<i>T. aestivum</i> subsp. <i>compactum</i>	14	<i>T. turgidum</i> subsp. <i>durum</i>
2	<i>T. aestivum</i> subsp. <i>macha</i>	52	<i>Triticum</i> (other tetraploids)
20	<i>T. aestivum</i> subsp. <i>spelta</i>	62	<i>Triticum</i> sp.
4	<i>T. aestivum</i> subsp. <i>sphaerococcum</i>	11	<i>Aegilops</i> sp.
102	<i>T. aestivum</i>	370	<i>S. cereale</i>
66	<i>Triticum</i> (diploids)		

### ***The Mac Key Collection of near-isogenic lines.***

The collection of NILs in wheat, oat, and barley has been developed by Professor James Mac Key at the Swedish University of Agricultural Sciences in Uppsala. The NILs carry resistance genes for several diseases of cereals as well as genes for different physiological traits. In the collection there are 120 lines of spring wheat (backcrossed to Prins) and 79 accessions of winter wheat (backcrossed to Starke II).

### ***The Nilsson-Ehle/Müntzing Inbred Rye Collection.***

This collection consists of 131 inbred lines derived from the rye cultivar Stål. Professor Herman Nilsson-Ehle at the Swedish Seed Association (Sveriges Utsädesförening) began developing this material in 1925. The project was later continued by professors Arne Müntzing (from 1938 to 1974) and Arne Lundqvist at the Institute for Genetics, Lund University.

---

***The collection of wild *Triticeae* species and local varieties.***

Comprising this collection are 1,286 accessions, which consists of wild and cultivated species from tribe *Triticeae*. There are samples of species within genera *Hordeum*, *Triticum*, *Secale*, *Aegilops*, *Elymus*, *Roegneria*, *Agropyron*, and *Brachypodium*.

The larger part of the material is *Hordeum* accessions. The collection is the result from a Swedish-Danish coöperation in *Triticeae*. The collection has been donated to NGB by Professor Roland von Bothmer at the Swedish University of Agricultural Sciences.

***Triticum* material in the collection.** There are 85 accessions of *T. aestivum* subsp. *aestivum*. All are landraces. One originates in Argentina, two in the former USSR (Tadjhikistan), seven in Pakistan, and the others have been collected in China. In this collection there also is one accession of *T. monococcum* subsp. *monococcum*, one accession of *T. turgidum* subsp. *durum*, four accessions of *Aegilops* spp., and two of *S. cereale*.

***The Haslund-Christensen Expedition to Central Asia.***

The material was collected in Afghanistan during the 1940s by the Haslund-Christensen expedition from Copenhagen University. This unique collection of about one hundred cereal accessions cannot be repatriated to the country of origin under present circumstances, and the NGB has taken long-term responsibility for the material. There are 63 accessions of *Triticum* sp. and nine of *S. cereale* in this collection.

***The Åberg Collection.***

During the years 1953–55, C. L. Behm collected material in Afghanistan, Kashmir, Tibet, and Iran. The collection was handed over to Professor Erik Åberg at the Swedish University of Agricultural Sciences, Uppsala, in 1955. Professor Åberg donated the material to NGB. The Åberg collection consists of about 1060 spike samples (herbarium) of *Hordeum*, *Triticum*, and *Avena*, as well as 53 seed accessions (of which none are *Triticum*). The material is of significant historical value, probably of great diversity, and will most likely be of importance for future research.

**ITEMS FROM THE UKRAINE****KHARKOV NATIONAL UNIVERSITY**

**Department of Plant Physiology and Biochemistry, Svoboda sq. 4, Kharkov, 61007, Ukraine.**

***Activation of the phytochrome system and status of phytohormones at vernalization in winter wheat seedlings.***

V.V. Zhmurko and O.A. Avksentyeva.

The speed of development in soft wheat is determined by three genetic systems: *Vrn* genes, which control vernalization; *Ppd* genes, which control of photoperiodical sensitiveness; and genes for early maturation (per se) (Stelmakh 1998). Today, the genetic effects of these systems are well known. However, effects of *Vrn* genes on physiological functions are unknown. Particularly, the possible participation of phytohormones and phytochromes in regulating of these genes expression is not examined. Phytohormones are known to ‘start’ entire morphogenetic processes. The possible mechanism of this process consists of depressing one or more genes. One hypotheses to explain the effects of phytochromes in

plants is that activation of phytochromes by red light determines the action of gene expression that takes place (Fedenko et al. 1999; Tarchevski 2002).

Based on these facts, we presume that expression of *Vrn* genes in soft wheat can occur as result of phytohormones and phytochromes actions. Until now, this question has not been addressed in the literature, although understanding the mechanisms of physiological regulation of gene expression of development wheat and mechanism of ontogenesis in plants is very important.

The winter wheat Mironovskaya 808, which has recessive *Vrn* genes, can not form spikes unless vernalized. Seedlings were vernalized for 60 days at 0–2°C with red (660 nm) and far-red (730 nm) light and out light (control). Phytohormones, gibberellin (GA), indoleacetic acid (IAA), cytokinin, and abscisic acid (ABA) activities were effected.

The results show that vernalization determines modifications in the level of phytohormones in winter wheat. Phytohormone activity effects growth (IAA and GA), decreasing until day 45 and increasing before the end of vernalization (day 60). Phytohormone activity that depressed the growth (ABA). No variation in cytokinin activity was observed.

Phytochromes are the main photoreceptor system of plants and control the regulation of many biochemical, physiological, and morphological processes (Fedenko et al. 1999). Vernalization determines the rate of development in winter wheat, the ability to flower. Changes in the dynamics of phytohormone activity in winter wheat seedlings regulate development. Most likely, these systems interact in the regulation of the vernalization processes.

The influence of phytochrome activation on GA activity show that red light inhibits GA activity on day 30 compared with the control and the far-red and red + far-red light treated plants. Red + far-red light had the greatest impact on GA activity in comparison to all other experimental treatments (Table 1).

IAA activity on day 30 of vernalization was the greatest with red + far-red light irradiation and lowest under far-red light irradiation compared with the untreated control seedlings. Phytohormone activity was reduced under red and far-red light until vernalization was complete (60 days). Activity increased in the control, but almost did not change under red + far-red light irradiation. Only IAA activity on day 60 was lower in the control than in the treated seedlings (Table 1).

Cytokinin activity on day 30 was the highest under far-red light and equal in all other treatments. During the next 15 days of vernalization until day 45, cytokinin activity increased in the control and seedlings treated with red light, but decreased in seedlings treated with far-red and red + far-red light. Changes in the cytokinin activity were insignificant (Table 1).

ABA activity after 30 days of vernalization under the influence of red and far-red light and in the control were nearly equal, however higher than ABA activity under the influence of red + far-red light. Up to day 45 of vernalization, ABA activity increased in all variants, but more in those treated with red + far-red light, somewhat less under the influence of red light, still less in control, and least under the influence of far-red light. Until the end of vernalization (day 60), the activity of ABA in the control and seedlings under the influence of red light continued to decrease, but increased slightly in seedlings under the influence of far-red light and red + far-red light (Table 1).

**Table 1.** Influence of red and far-red light on change of the contents of phytohormones in the winter wheat seedlings in the time of vernalization. Values are % of control.

Variant	IAA	ABA	CK	GA
<b>30-DAY VERNALIZATION</b>				
Control	122 ± 09	29 ± 3	85 ± 7	81 ± 6
Red (660 nm)	135 ± 11	34 ± 4	85 ± 7	71 ± 5
Far-red (730 nm)	104 ± 08	30 ± 3	103 ± 8	84 ± 7
Red + far-red	148 ± 13	41 ± 4	87 ± 6	115 ± 9
<b>45-DAY VERNALIZATION</b>				
Control	109 ± 07	43 ± 4	91 ± 7	55 ± 4
Red	130 ± 11	46 ± 3	89 ± 7	87 ± 7
Far-red	117 ± 08	51 ± 3	98 ± 8	48 ± 4
Red+far-red	113 ± 10	72 ± 5	79 ± 7	70 ± 6
<b>60-DAY VERNALIZATION</b>				
Control	122 ± 09	69 ± 7	96 ± 7	38 ± 2
Red	65 ± 05	49 ± 4	83 ± 7	31 ± 3
Far-red	96 ± 08	37 ± 3	83 ± 7	32 ± 3
Red+far-red	113 ± 09	44 ± 3	89 ± 7	29 ± 2

The phytochrome activation system during vernalization determines changes in the activity of phytohormones. We propose that metabolic and phytohormonal processes take part expression of genes *Vrn* by activation of phytochromes. However, subsequent researches are necessary for definition of expression mechanisms.

### References.

- Fedenko EP, Agamova SP, and Koksharova TA. 1999. Success of Cont Biology 119 (1):56-59.  
 Stelmakh AF. 1998. Genetic systems regulation flowering response in wheat: Prospect for Global improvement. Kluwer Academic Publishers, the Netherlands. Pp. 491-501.  
 Tarchevski IA. 2002. Signal system of plant cells. Science, Moscow. 293 p.

## INSTITUTE OF PLANT PRODUCTION N.A. V.YA. YURJEV Moskovsky prospekt, 142, 61060, Kharkiv, Ukraine.

### *Harmful flies (Diptera) in wheat field agrocoenosis.*

Yu.G. Krasilovetz, N.V. Kouzmenko, S.I. Popov, and V.A. Tzyganko.

An important trend in ecological orientation of farming is to fulfill a complex of protective measures for reducing insect damage. Our studies are aimed at the reduction of harmful effect on winter wheat plants caused by *Dipteran* flies using some agronomic management methods that are based on growing resistant cultivars, optimizing crop-rotation systems and forecrops, mineral nutrition, and monitoring of dates and rates of planting. The studies were conducted at the Experimental Farm of the Plant Production Institute V.Ya. Yurjev (Eastern Forest-Steppe of Ukraine) during 2001–04. The farm has a typical deep-humus, chernozem on loess soil. The agrochemical indices of the plowing layer are humus, 5.38 %; mobile nitrogen forms, 17.8 mg/100 g of soil (average); phosphorus, 16.3 mg/100 g of soil; and potassium, 13.2 mg/100 g of soil.

### Results.

**Forecrops.** During 2001–04, the forecrops of winter wheat were black fallow (manure 30 t/ha + (NPK)<sub>30</sub> + N<sub>30</sub>) and dried peas (manure after effect 30 t/ha + (NPK)<sub>30</sub> + N<sub>30</sub>). Total tillering and stem number/m<sup>2</sup> at tillering stage (the third stage of organogenesis of winter wheat according to F.M. Koupermann) did not vary (Table 1, p. 168). For example, the black fallow and winter wheat after dried peas treatment, total tillering was 4.3 and 4.1, respectively, and stem number/m<sup>2</sup> as 1.8 and 1.7 x 10<sup>3</sup>, respectively. Black fallow is regarded to be the best forecrop for winter wheat compared with peas. To obtain the optimal number of productive spike-bearing stems (550–600 stems/m<sup>2</sup>), winter wheat is planted at different rates; e.g., in black fallow, 4.0 x 10<sup>9</sup> germinating seeds/ha and after peas, 5.0 x 10<sup>9</sup> germinating seeds/ha. Over the years of the study, average total shoot damage in winter wheat at the tillering stage by larvae of various *Diptera* spp. on black fallow was by 1.4 time less than that of dried peas. This index was 5.2 % on black fallow and 7.5 % after peas. *Oscinella* spp. dominated and damaged an average of 70.6 % of the shoots on black fallow and 59.5 % of shoots in winter wheat after dried peas. Less damage by *Opomyza florum* was observed, 29.4 % on black fallow and 40.5 % after peas. In 2004, *Phorbia secures* caused 0.2 % shoot damage. Averaged over the 3 experimental years, winter wheat grain yield on black fallow (6.5 t/ha) surpassed that after peas (5.5 t) by 1.0 t/ha.

**Cultivar.** On black fallow (manure 30 t/ha + (NPK)<sub>30</sub> + N<sub>30</sub>), total tillering in the winter wheat cultivar Donetsk'ka 48 surpassed that of the control Kharus by 13.7 %. Total tillering was estimated at 5.2 for Donetsk'ka 48 and 4.3 for Kharus. Stem number/m<sup>2</sup> in Donetsk'ka 48 and Kharus was similar, 1.8 x 10<sup>3</sup> stems/m<sup>2</sup>. According to the average indices, total damage to the stems by fly larva in Kharus was by 1.3 time less than that in Donetsk'ka 48. Grain yield in Donetsk'ka 48 (5.7 t/ha) was inferior to that of Kharus (7.1 t/ha) by 1.4 t/ha.

**Fertilizer.** The effect of fertilizer on total tillering (in case of black fallow) was not sufficient. The number of stems/m<sup>2</sup> in the blocks with manure a application of 30 t/ha + (NPK)<sub>60</sub> + N<sub>30</sub> was 1.9, lower than that of manure 30 t/ha + (NPK)<sub>30</sub> + N<sub>30</sub> (1.8), with manure at 30 t/ha, (1.9), without fertilizers (1.6 x 10<sup>3</sup> pcs/ha. Thus, fertilizer increased this index by 11.1–15.8 % compared to the block without fertilizers. On average, the lowest level of damage to the shoots by fly larva was observed in the block treated with 30 t/ha manure (3.1) compared with the block without fertilizers (5.6 % damage).

**Table 1.** Winter wheat damage caused by *Diptera* and grain yield depending on agricultural cultivation practices during 2001–04.

Treatment	Total tillering	Stems/ m <sup>2</sup> (x 10 <sup>3</sup> )	Shoot damage by fly larvae at the tillering stage			Grain yield (t/h)			
			total	<i>Oscinella</i> spp.	<i>Opomiza</i> <i>florum</i>				
						2001	2002	2003	Average
<b>FORECROP</b>									
Black fallow	4.3	1.8	5.2	1.2	0.5	5.6	7.9	6.0	6.5
Dried peas	4.1	1.7	7.5	2.2	1.5	3.6	6.9	6.0	5.5
LSD <sub>05</sub>						1.2	2.3	0.5	
<b>CULTIVAR</b>									
Kharus	4.3	1.8	5.6	1.3	0.7	7.3	7.9	6.0	7.1
Donetz'ka 48	5.2	1.8	7.2	1.0	0.8	4.8	6.3	6.1	5.7
LSD <sub>05</sub>						1.0	1.9	0.3	
<b>FERTILIZER</b>									
No fertilizer	4.6	1.6	5.6	1.6	1.2	4.1	7.3	5.9	5.8
Manure 30 t/ha	5.0	1.9	3.1	0.8	0.4	4.2	7.6	6.1	6.0
Manure + (NPK) <sub>30</sub> + N <sub>30</sub>	4.3	1.8	4.9	1.2	0.7	4.7	7.9	6.0	6.2
Manure + (NPK) <sub>60</sub> + N <sub>30</sub>	4.8	1.9	6.8	2.6	0.4	5.6	7.2	5.8	6.2
LSD <sub>05</sub>						0.2	1.0	0.3	
<b>SOWING DATE</b>									
I – 10.09	4.5	1.9	5.0	1.0	0.7	4.9	7.9	6.0	6.3
II – 20.09	4.4	1.9	4.2	0.7	0.3	6.1	7.7	5.8	6.5
III – 30.09	3.8	1.7	2.5	0.1	0.1	7.2	7.1	6.2	6.8
LSD <sub>05</sub>						0.7	1.6	0.4	
<b>SOWING RATE</b>									
4.0	4.8	1.8	7.1	0.5	0.7	4.7	7.9	6.1	6.2
5.0	4.3	2.2	5.8	1.1	1.0	4.9	8.5	6.4	6.6
LSD <sub>05</sub>						2.4	2.4	0.4	

According to the average data, a manure application at a rate of 30 t/ha increased winter wheat grain yield by 0.2 t/ha. Manure use at the rate of 30 t/ha (NPK)<sub>30</sub> + N<sub>30</sub> increased yield by 0.4 t/ha. In the block with 30 t/ha of manure (NPK)<sub>60</sub> + N<sub>30</sub>, the yield improved by 0.4 t/ha compared with the block with no fertilizers. In areas of high soil fertility and increased phosphorus-potassium, the additional application of manure at 30 t/ha and (NPK)<sub>60</sub> or (NPK)<sub>30</sub> did not contribute to an increase in grain yield.

**Sowing date.** In the black fallow treatment (manure 30 t/ha + (NPK)<sub>30</sub> + N<sub>30</sub>), total tillering in winter wheat at the first (10 September) and second (20 September) sowing dates surpassed that at the third date (30 September) by 13.6–15.6 %. Total tillering was 4.5 at the first date, 4.4 at the second, and 3.8 at the third. When the sowing date was much later, stem number/m<sup>2</sup> was reduced from 1.9 x 10<sup>3</sup> to 1.7 x 10<sup>3</sup>. At tillering, total damage to the shoots by fly larva that had overwintered was gradually reduced from the first (5.0 %) to the third sowing dates (2.5 %). The average grain yield in winter wheat sown at the third date (6.8 t/ha) surpassed that of the second (6.5 t/ha) and first dates (6.3 t/ha) by 0.3 and 0.5 t/ha, respectively.

**Sowing rate.** In black fallow (manure 30 t/ha + (NPK)<sub>30</sub> + N<sub>30</sub>) at the sowing rate of 4.0 x 10<sup>6</sup> germinating seeds/ha, total tillering was 4.8. At a rate of 5.0 x 10<sup>6</sup> germinating seeds the tillering rate was 4.3. At the 5.0 x 10<sup>6</sup> seeding rate, stem number increased to 2.2 x 10<sup>3</sup>/m<sup>2</sup> compared to that at 4.0 x 10<sup>6</sup> (1.8 x 10<sup>3</sup> seeds/m<sup>2</sup>). Total damage of to the winter wheat shoots by fly larva in these treatments ranged between 5.8–7.1 %. Grain yield in winter wheat fields at a sowing rate of 5.0 x 10<sup>6</sup> (6.6 t/ha) germinating seeds surpassed that at 4.0 x 10<sup>6</sup> by 0.4 t/ha.

**Identifying sources and donors of genes for resistance to covered smut of winter wheat in Ukraine.**

V.P. Petrenkova, S.V. Rabynovich, I.M. Chernyaeva, and L.M. Chernobai.

Screening of 400-650 cultivars and lines of winter wheat during 2001–04 identified sources of resistance to covered smut within a group of modern world wheats and breeding material adapted to the local conditions. Analysis of the breeding material shows that only 7–10 % of winter wheat lines is characterized by resistance to covered smut (damage less than 10 %). Because of the low level of genetic protection in breeding lines, introducing new sources of disease resistance into breeding programs is important.

Covered smut is an extremely harmful disease and chemical seed pretreatment is needed. These chemicals are rather aggressive and can harm natural soil organisms. The pathogenic population of covered smut in Ukraine is comprised of two species, *T. caries* and *T. laevis*, with a wide range of the races. At present in the central part of Ukraine, the highly virulent race 37 has been replaced completely by the less virulent race 32 (Krivchenko 1984). In the south, the highly virulent race 40 has been succeeded by the less virulent race 11. In the eastern part of the Forest-Steppe, race 11 dominates (Radchenko 2003). As a result of significant changes in the race composition of covered smut in Ukraine, resistance genes *Bt1*, *Bt2*, *Bt3*, and *Bt7* have lost their effectiveness, but *Bt5*, *Bt10*, *Bt11*, *Bt14*, *Bt15*, and *Bt16* still are highly effective. In the Kharkiv Oblast, our data indicate that the pathogen population is predominantly represented by less virulent races 3, 5, and 16 of *T. caries*, the more aggressive races controlled by the numerous well-known *Bt* genes.

Winter wheat entries were planted in the infection nurseries of the Division for Plant Immunity to Diseases and Pests of our institute. To study resistance to covered smut, seed samples are inoculated with the spores of the covered smut pathogen from the local population and sown in a special nursery (Babayants et al. 1998). To control the quality of the inoculation and the conditions of its expression and spread, 20 susceptible cultivars chosen according previous data were sown in the infection nurseries.

In 2001–04, 396 selected and 566 collection cultivars and lines of winter wheat were studied for resistance to covered smut in the infection nursery. Based on plant damage in the susceptible controls, we identified sources of resistance within the range of 45–87 %. These resistant lines include winter wheats from the U.S. (Rod, Idaho 364, McVicar, CO900134, CO900166, WRB+86036, and T 96V2112), Winridge (*Bt1*, *Bt4*, *Bt6*, *Bt9*, and *Bt10*, pedigree Madsen (VPM/Moisson//2\*HILL 81 (Yamhil/Hyslop (*Bt1* and *Bt4*), and two lines singled out from an analogous cross in made in Oregon (resistance lasting for more than 10 years). The smut resistance in these lines was inherited not only from Hyslop, which is resistant to covered smut in our local conditions, but also from the French line VPM1 (an *Ae. ventricosa*-derived line) (Dolgova et al. 1996).

We also identified some modern Ukrainian cultivars with good agronomic traits that were resistant to covered smut including Lutescens 779/83, Erythrosperrum 24220, Lutescens 2690, Lutescens 8589, Erythrosperrum 26221, Columbia, and Ferugineum 220/85 (with effective genes *Bt15* and *Bt16*). Ferugineum 220/85 is characterized by resistance to loose smut and brown rust and has high productivity and grain quality.

Among the lines with new, highly effective genes of resistance derived from the *Aegilops*, the crosses ‘*Ae. juvenalis*/6\*Chris//Selkirk’, ‘*Ae. ventricosa*/*T. turgidum* subsp. *durum*//3\*Selkirk’, ‘*Ae. tauschii*/9\*Selkirk’, ‘*T. aestivum* subsp. *macha*/9\*Selkirk’ are of interest.

Three lines released from our institute that can be used as a source of resistance are Erythrosperrum 16-01, Erythrosperrum 36-01, and Lutescens 157-01. These lines were selected for smut resistance in 2002 and remained resistance during a 2004 epidemic with a 4–9 % degree of infection.

We made test crosses in order to evaluate the cultivars Charmany and Idaho 352 for resistance to covered smut (Table 2). Resistance of these cultivars during all years of the study was very high, similar to that of the lines with the highly effective resistance genes *Bt5* and *Bt9–Bt17*, which are effective against the local population *T. caries*. The hybrids derived from these resistant cultivars were resistant or highly resistant, indicating the presence of dominant genes in Charmany and Idaho 352 (Table 2). In the  $F_2$  of hybrids from crosses between the resistant cultivar Charmany and susceptible cultivars Kharkivs’ka 96 and Churaivna, the ratio of resistant and susceptible plants corresponded to the

**Table 2.** Segregation of  $F_2$  hybrids for resistance to covered smut in crosses with the cultivars Charmany and Idaho 352 in 2004.

Cross	Resistance score			Phenotypic ratio in $F_2$ populations		$X^2$	$P$	No, of genes
	Parent 1	Parent 2	$F_1$	observed	expected			
Charmany/Echo	9	2	8	84:21	13:3	0.11	0.50-0.75	2
Charmany/Snezhinka	9	2	9	105:12	15:1	3.21	0.05-0.07	2
Charmany/Churaivna	9	1	8	78:15	13:3	0.42	0.50-0.75	2
Charmany/Kharkivs'ka-96	9	2	7	39:6	13:3	0.87	0.25-0.50	2
Idaho 352/Echo	8	2	8	57:6	15:1	1.15	0.25-0.50	2
Idaho 352/Snezhinka	8	2	8	99:9	15:1	0.80	0.25-0.50	2
Idaho 352/Zolotava Nosovs'ka	8	2	8	66:6	15:1	0.53	0.25-0.50	2

expected 13:3 ratio. Thus, the resistance in Charmany is controlled by two independent genes, one dominant and one recessive. In  $F_2$  of the cross combination between Charmany and Snezhinka, we observed segregation in the ratio of 15:1, which suggests the presence of two independent dominant genes. In crosses between the resistant cultivar Idaho 352 and three susceptible cultivars (Echo, Snezhinka, and Zolotava Nosivs'ka), the ration of resistant to susceptible plants corresponded to the expected 15:1 ratio, indicating two dominant genes for resistance in Idaho 352. Because we did not recover susceptible plants in the  $F_2$  in crosses between Idaho 352 and Kharkivs'ka 96 and Idaho 352 and Churaivna, possibly because of insufficient sampling or elimination of plants in the given class at the seedling stage, we did not make any conclusions concerning to these hybrids.

In conclusion, Charmany and Idaho 352 are the donors of resistance to the local population of covered smut and possess two independent genes; Charmany has one dominant and one recessive gene and Idaho 352 has two dominant genes.

## References.

- Babayants LT, Meshterkhazhi A, Bekhter F, et al. 1998. Methods of selection and evaluation of wheat and barley resistance to diseases. Prague, Czech Republic. 321 pp.
- Dolgova GM, Chernyaeva IN, and Afonskaya GG. 1996. Original material in breeding wheat for resistance to covered smut. Methodologic grounds of formation, management and use of plant genetic resources' collections. **In:** Proc Internat Symp, Kharkov, 2–4 October, 1996. Kharkov. p. 43.
- Krivchenko VI. 1984. Resistance to the pathogens of smut diseases in grain ear-bearing. M Kolos. 304 pp.
- Radchenko LM. 2003. Covered smut on winter wheat and the substantiation of immunologic methods of protection. Student Thesis in Agriculture, Kyiv. 140 pp.

## ITEMS FROM UNITED KINGDOM

### JOHN INNES CENTRE

Norwich Research Park, Colney Lane, Norwich NR4 7UH, United Kingdom.

### *Genetics of resistance of wheat to Septoria tritici blotch.*

James Brown, Lia Arraiano, and Laetitia Chartrain.

We have recently completed a industrial LINK project on Breeding for Resistance to *S. tritici*, supported by the Department for the Environment, Food and Rural Affairs and six plant breeding companies with U.K. interests. We have

discovered that many of the most widely-used sources of Septoria resistance in world wheat breeding have the gene *Stb6*. The widespread distribution of this gene limits the scope for transgressive segregation of resistance and points to the need to use a greater range of resistance genes. We have identified and mapped four new genes for resistance to Septoria, *Stb9* in several European spring wheat cultivars; *Stb10* and *Stb12* in Kavkaz-K4500, an especially important source of resistance; and *Stb11* in TE9111, a Portuguese breeding line that is the most resistant modern European wheat known. Through an associated genetic analysis, we also have shown that many genes, dispersed over the chromosomes of wheat, promote partial resistance to Septoria.

We are now beginning a new LINK project, Improved Resistance to *S. tritici* in Superior Varieties, in which we will quantify the contributions to disease reduction in the field of Septoria resistance genes identified in the previous LINK project and investigate the interaction of Septoria resistance with other plant traits important to U.K. and European wheat breeders.

### ***Fusarium and eyespot diseases of cereals.***

Paul Nicholson, Liz Chandler, Natalie Chapman, Richard Draeger, Nick Gosman, Wendy Monger, Andy Steed, and Martha Thomsett.

The study of the genetic basis of resistance to FHB in winter wheat is continuing. The resistance of Arina and WEK0609 has been analyzed and mapping and QTL analysis of resistance of these populations is nearing completion. Fine mapping of the *T. aestivum* subsp. *macha* 4A FHB resistance is ongoing and is being combined with gene-expression studies to identify candidate resistance genes. Host-pathogen interaction is being studied in detail for infection of Arina and Riband by *F. culmorum*. Expression of wheat PR genes and fungal toxin-biosynthesis genes is being determined for the two hosts during infection and colonization of wheat spikes. A collaborative project is underway to assess the level of FHB resistance among U.K. wheat cultivars and to introduce and pyramid FHB from diverse sources to improve the level of resistance among winter wheat cultivars in the U.K. SSR analysis of U.K. and European wheats indicates the absence of any of the common FHB-resistance QTL of Chinese origin among this germ plasm lines are being developed to determine the combining ability of selected FHB QTL to identify the best combinations for use in breeding programs. Molecular diagnostics are being used to study effects of, and interactions between, *Fusarium* isolates of different chemotype on different cereal hosts. Molecular diagnostics also have revealed that the U.K. wheat crop is exposed to a more diverse array of chemotypes than that in the U.S. In addition to studies on FHB, mapping and molecular studies of two eyespot resistance genes (*Pch1* and *Pch2*) are continuing.

### ***Genetic biodiversity of adult-plant resistance to yellow rust in wheat.***

Lesley A. Boyd, Clare Lewis, Muge Sayar, James Melichar, Luke Jagger, and Hale Tufan.

A number of QTL for APR to yellow (stripe) rust have been identified in the U.K. wheat cultivar Claire and within the Claire pedigree. Mapping work also is underway to identify the QTL for a source of partial APR to yellow rust in the cultivar Guardian.

The dissection of genetic biodiversity for yellow rust APR in U.K. wheat cultivars will be extended to include a comparison to biodiversity in Turkish wheats as part of a new collaboration between H-J. Braun (CIMMYT, Turkey) and M.T. Sayar (Bogazici University, Istanbul, Turkey).

### ***Novel sources of resistance to biotrophic fungal pathogens in wheat.***

James Melichar and Lesley A. Boyd.

A number of mutants, generated by gamma-radiation in the U.K. cultivar Guardian, were originally selected in the field for enhanced resistance to yellow rust. This enhanced resistance was shown not to express in seedlings, but to be developmentally regulated, expressing at adult plant growth stages. A microscopic-staining procedure has been developed in the group that allows detailed histological examination of yellow rust development in adult plant tissue. Using

this methodology, the partial APR in Guardian has been shown to restrict sporulation, but this resistance is not associated with the release of hydrogen peroxide by the plant, a response common to race-specific resistance. However, the enhancement of resistance, due to mutation, is associated with the production of hydrogen peroxide.

In addition to the enhancement of resistance to yellow rust in adult plants, a number of the mutants also exhibit enhanced resistance to leaf rust and/or powdery mildew. Mapping populations have been developed for Guardian and two of the mutants, and these will be used to locate both the partial yellow rust APR in Guardian, the mutations responsible for the enhancement of yellow rust resistance, and the mutations conferring resistance to leaf rust and powdery mildew.

### ***Factors affecting yellow rust infection efficiency.***

Ruth MacCormack and Lesley A. Boyd.

A new program in the laboratory of L.A. Boyd examines the early stages of yellow rust infection to determine what factors optimize infection efficiency of this fungal pathogen. Having identified the physiological factors that the pathogen requires to successfully enter the plant through open stomata, phenotypic screens will be established to look for genetic variation within wheat for infection efficiency.

### ***An immortal population of mutagenized spring wheat.***

Simon Orford, Pauline Stephenson, and Robert Koebner.

As part of our contribution to the Wheat Genetic Improvement Network (see AWN 50:192), we are developing an immortal population of EMS-mutagenized spring wheat cultivar Paragon by single-seed descent. The initial  $M_1$  population numbered ~ 3,500 individuals, from which two  $M_2$  seeds/ $M_1$  plant were sown. The population is currently (spring-summer 2005) being advanced from  $M_3$  to  $M_4$  as ~ 7,000 independent lines. From the  $M_6$ , we intend to field multiply the lines and make them available to collaborators for gene discovery and functional gene analysis.

### ***Homoeologous silencing in hexaploid wheat.***

Andrew Bottley and Robert Koebner.

Our SSCP-based analysis of patterns and frequency of homoeolog silencing in wheat continues to surprise. We are working with single-copy EST sequences located to homoeologous group under the NSF wheat EST program, comparing amplicon patterns generated from cDNA templates from both root and leaf tissue. Globally, around 15 % of the loci are nontranscribed, but we have noted a significant frequency of cases where in the presence of additional doses of a chromosome (as are present in the nullisomic-tetrasomic stocks), a homoeolocus silenced in the euploid condition is transcribed. To avoid noncomparability between genomic and cDNA profiles, we are using the rice genome sequence to target amplicons lacking intron sequence.

### **Publications.**

- Bourdon V, Wickham A, Lonsdale D, and Harwood W. 2004. Additional introns inserted within the luciferase reporter gene stabilise transgene expression in wheat. *Plant Sci* 167:1143-1149.
- Castro AM, Vasicek A, Ellerbrook C, Gimenez DO, Tocho E, Tacaliti MS, Clua A, and Snape JW. 2004. Mapping quantitative trait loci in wheat for resistance against greenbug and Russian wheat aphid. *Plant Breed* 123:361-365.
- Chartrain L. 2004. Genes for isolate-specific and partial resistance to septoria tritici blotch (*Mycosphaerella graminicola*) in wheat. PhD Thesis, University of East Anglia. 151 pp.
- Chartrain L, Berry ST, and Brown JKM. 2005. Resistance of the wheat line Kavkaz-K4500 L6.A4 to Septoria tritici blotch controlled by isolate-specific resistance genes. *Phytopath* (In press).
- Chartrain L, Brading PA, Makepeace JC, and Brown JKM. 2004. Sources of resistance to Septoria tritici blotch and implications for wheat breeding. *Plant Path* 53:454-460.

- Chartrain L, Brading PA, Widdowson JP, and Brown JKM. 2004. Partial resistance to *Septoria tritici* blotch (*Mycosphaerella graminicola*) in wheat cultivars Arina and Riband. *Phytopath* 94:497-504.
- Chartrain L, Brading PA, and Brown JKM. 2005. The presence of the *Stb6* gene for resistance to *Septoria tritici* blotch (*Mycosphaerella graminicola*) in cultivars used in wheat breeding programmes world-wide. *Plant Path* (In press).
- Chartrain L, Joaquim P, Berry ST, Arraiano LS, Azanza F, and Brown JKM. 2005. Genetics of resistance to *Septoria tritici* blotch in the Portuguese wheat breeding line TE 9111. *Theor Appl Genet* (In press).
- Dawson WAJM, Jestoi M, Rizzo A, Nicholson P, and Bateman GL. 2004. Field evaluation of fungal competitors of *Fusarium culmorum* and *Fusarium graminearum*, casual agents for ear blight of winter wheat, for the control of mycotoxin production in grain. *Biocontrol Sci Tech* 14:783-799.
- Foote TN, Griffiths S, Allouis S, and Moore G. 2004. Construction and analysis of a BAC library in the grass *Brachypodium sylvaticum*: its use as a tool to bridge the gap between rice and wheat in elucidating gene content. *Funct Integr Genomics* 4:26-33.
- Foulkes MJ, Sylvester-Bradley R, Worland AJ, and Snape JW. 2004. Effects of a photoperiod-response gene *Ppd-D1* on yield potential and drought resistance in UK winter wheat. *Euphytica* 135:63-73.
- Gosman N, Chandler E, Thomsett M, Draeger R, and Nicholson P. 2005. Analysis of the relationship between parameters of resistance to *Fusarium* head blight and *in vitro* tolerance to deoxynivalenol of the winter wheat cultivar WEK0609. *Eur J Plant Path* 111:57-66.
- Guilleroux M, and Osbourn A. 2004. Gene expression during infection of wheat roots by the 'take-all' fungus *Gaeumannomyces graminis*. *Mol Plant Path* 5:203-216.
- Hayden MJ, Stephenson P, Logojan AM, Khatkar D, Rogers C, Koebner RMD, Snape JW, and Sharp PJ. 2004. A new approach to extending the wheat marker pool by anchored PCR amplification of compound SSRs. *Theor Appl Genet* 108:733-742.
- Jennings P, Coates ME, Walsh K, Turner JA, and Nicholson P. 2004. Determination of deoxynivalenol- and nivalenol-producing chemotypes of *Fusarium graminearum* isolated from wheat crops in England and Wales. *Plant Path* 53:643-652.
- Jennings P, Coates ME, Turner JA, Chandler EA, and Nicholson P. 2004. Determination of deoxynivalenol and nivalenol chemotypes of *Fusarium culmorum* isolates from England and Wales by PCR assay. *Plant Path* 53:182-190.
- Mohler V, Lukman R, Ortiz-Islas S, William M, Worland AJ, van Beem J, and Wenzel G. 2004. Genetic and physical mapping of photoperiod insensitive gene *Ppd-B1* in common wheat. *Euphytica* 138:33-40.
- Nicholson P, Simpson DR, Wilson AH, Chandler E, and Thomsett M. 2004. Detection and differentiation of trichothecene and enniatin-producing *Fusarium* species on small-grain cereals. *Eur J Plant Path* 110:503-514.
- Prins R, Ramburan VP, Pretorius ZA, Boyd LA, Boshoff WHP, Smith PH, and Louw JH. 2005. Development of a doubled haploid mapping population and linkage map for the bread wheat cross Kariega x Avocet S. *S Afr J Plant Soil* 22:1-8.
- Ramburan VP, Pretorius ZA, Louw JH, Boyd LA, Smith PH, Boshoff WHP, and Prins RA. 2004. Genetic analysis of adult plant resistance to stripe rust in the wheat cultivar Kariega. *Theor Appl Genet* 108:1426-1433.
- Ribeiro-Carvalho C, Guedes-Pinto H, Igrejas G, Stephenson P, Schwarzacher T, and Heslop-Harrison JS. 2004. High levels of genetic diversity throughout the range of the Portuguese wheat landrace 'Barbela'. *Ann Bot* 94:699-705.
- Rodrigues P, Garrood JM, Shen Q-H, Smith PH, and Boyd LA. 2004. The genetics of non-host disease resistance in wheat to barley yellow rust. *Theor Appl Genet* 109:425-432.
- Simon MR, Worland AJ, and Struik PC. 2004. Influence of plant height and heading date on the expression of the resistance to *Septoria tritici* blotch in near isogenic lines in wheat. *Crop Sci* 44:2078-2085.
- Smith PH, Howie JA, Worland AJ, Statford R, and Boyd LA. 2004. Mutations in wheat exhibiting growth-stage-specific resistance to biotrophic fungal pathogens. *Mol Plant-Microbe Interact* 17:1242-1249.
- Toth B, Mesterhazy A, Nicholson P, Teren J, and Varga J. 2004. Mycotoxin production and molecular variability of European and American isolates of *Fusarium culmorum*. *Eur J Plant Path* 110:587-599.
- Turner AS, Bradburne RP, Fish L, and Snape JW. 2004. New quantitative trait loci influencing grain texture and protein content in bread wheat. *J Cereal Sci* 40:51-60.
- Verma V, Foulkes MJ, Worland AJ, Sylvester-Bradley R, Caligari PDS, and Snape JW. 2004. Mapping quantitative trait loci for flag leaf senescence as a yield determinant in winter wheat under optimal and drought-stressed environments. *Euphytica* 135:255-263.
- Vorontsova M, Shaw P, Reader S, and Moore G. 2004. Effect of 5-azacytidine and trichostatin A on somatic centromere association in wheat. *Genome* 47:399-403.
- Xu X-M, Parry DW, Edwards SG, Cooke BM, Doonan FM, van Maanen A, Brennan JM, Monaghan S, Moretti A, Tocco G, Mule G, Hornok L, Giczey G, Tatnell J, Nicholson P, and Ritieni A. 2004. Relationship between the incidences of ear and spikelet infection of *Fusarium* ear blight in wheat. *Eur J Plant Path* 110:959-971.

---

ITEMS FROM THE UNITED STATES OF AMERICA

---

**GEORGIA / FLORIDA****GEORGIA EXPERIMENT STATION / UNIVERSITY OF GEORGIA  
Griffin, GA 30223-1197, USA.**

J.W. Johnson, R.D. Barnett, G.D. Buntin, and Z. Chen.

The 2004 Georgia winter wheat crop was grown on about 330,000 planted acres, a decrease of 13% from the previous year. Oat acreage was 80,000 acres, a 20 % decrease from last year. Planted acres planted to rye, 230,000, were 18% less than last year. The condition of the small grain crops after the dry conditions were much better than anticipated. Yields of wheat grown by top producers were around 6000 kg/ha. The growing season was characterized by mild weather and dry conditions during the winter and spring. Lack of vernalization was a problem for late maturing cultivars. Very dry conditions during the late spring contributed to the low levels of diseases.

***Breeding.***

**Wheat. Vigoro McIntosh** is a new cultivar developed by the University of Georgia and the University of Florida. Derived from a backcross 'Gore\*2/T83267', the pedigree of Gore is 'Stacy/Coker 797' and the pedigree of T83267 is 'Coker 916/Florida 302'. McIntosh is a medium-late maturing, white chaffed, medium-tall height line. McIntosh matures on average 2 days later than AGS 2000 in Georgia. McIntosh is resistant to currently biotypes of Hessian fly and moderately resistant to races of powdery mildew, and susceptible to leaf rust in Georgia. The cultivar is resistant to WSBMV and stripe rust.

**Oat. Horizon 321** is a new winter oat cultivar that has considerable potential for both grain and forage production in the Southeast. This line originated from a cross made in 1997 between a Coker breeding line (Ck92Ab719) and Horizon 314 at the North Florida Research and Education Center at Quincy, Florida, and has the following pedigree: Coker 75-26/CI8341/4/Coker 76-19/Coker 75-27\*2/3/Coker 75-26//Coker 76-23/CI8322/5/Horizon 314. Horizon 321 was tested experimentally as FL9708-P37. Horizon 321 is a mid-season winter oat with excellent grain and forage production potential, good test weight and excellent disease resistance. The cultivar most closely resembles its Horizon 314 parent but is about 3 days earlier in heading and has better disease resistance particularly to stem rust. Horizon 321 has white seed similar to Horizon 314 and is medium in height similar to Horizon 474 and about 6 inches shorter than Harrison. The cultivar has very good crown and stem rust resistance to the current races.

**Triticale. Monarch** (tested experimentally as FL94128-Y1-A8) resulted from a cross made in the spring 1994 at the North Florida Research and Education Center at Quincy, FL, with the following pedigree: M93-188/FL87TH4004-3-N3-R1-S1-T1. M93-188 is a line obtained from Dr. Robert Metzger, USDA, located at Oregon State University. M93-188 had the following pedigree: CT583.81//A876/M76-6269. FL87TH4004-3-N3-R1-S1-T1 is a Florida advanced line with the pedigree 'Florico/NF117'. NF117 was a winter breeding line from the Noble Foundation at Ardmore, OK. Across the three locations Monarch averaged 4,567 lbs of grain/acre compared to several checks in the trial (AGS 2000 wheat 4,558 lbs/acre, Florico 4,263 lbs/acre, Arcia 3,393 lbs/acre, and Sunland 3,296 lbs/acre) . Monarch was ranked 6th in yield among the 42 entries across locations. At Quincy, Monarch headed 3 days later than Sunland but was 4 days later in heading at Marianna.

**Rye. AGS 104** is a rye for early season forage productions that will work well in blends with ryegrass for long season forage production with excellent rust resistance. In appearance, AGS 104 mostly closely resembles Wrens 96 and is slightly later than Wrens 96 in maturity, but similar in height and seed appearance. AGS 104 has been released exclusively to AGSouth Genetics.

### *Cytogenetics.*

The effect of introgression of rye chromosome arm from the absence of a corresponding wheat chromosome arm has not been fully studied. The agronomic and milling and baking quality effects of the individual wheat and rye chromosome 1 arms in translocations, substitutions, and nontranslocation lines were determined. Chromosome 1RS significantly increased grain yield depending upon the source of rye chromatin. All translocations and substitutions involved with 1RL had a negative effect on agronomic performance and had significantly higher protein content. The 1RS translocations increased alkaline water retention capacity (AWRC). The baking quality was not dependent on 1RS source in wheat-rye translocations but was dependent upon the wheat chromatin that was replaced by the rye chromatin. The 1RS translocations can be used to improve grain yield when the source is carefully selected from different wheat genetic background. The translocation T1RS·1BL gave the optimum for agronomic performance, whereas T1RS·1AL was the best for milling and baking quality.

**Effect of the T1DL·1RS translocation.** The influence of the T1DL·1RS genotype on agronomic performance and end-use quality was determined in two crosses. Grain yield and test weight of the 'Kanto/Gabo' (T1DL·1RS) were significantly lower than nonsiblings, but no significant differences were observed in the cross 'Jaypee/Gabo'. The effects of the translocation for quality traits were undesirable for cookie quality. The effects of the translocation on agronomic performance were modified by wheat genetic background, while milling and baking qualities were less affected.

### *Quality.*

The particles sizes of soft and hard wheat flours at isothermal temperatures exhibited trimodal size distributions. Isolated starch and gluten indicated that the first and second modes were mainly associated with starch granules, while the third mode was related to gluten and particle clusters. Soft wheat flours showed higher volume fractions in the first and second modes indicating more dissociated starch granules. Hard wheat flours had a higher volume fraction of particles ranging above 120 µm at elevated temperatures. Thus, the difference in size of single particles and starch protein aggregates, when comparing soft and hard wheat flour is due to the strength of starch protein interactions.

### *Publications.*

- Barnett RD, Pfahler PL, Blount AR, and Johnson JW. 2004. Registration of FL-SYNT tetraploid spring rye germplasm. *Crop Sci* 44:1884-1885.
- Kim W, Choi SG, Kert WL, Johnson JW, and Gaines CS. 2004. Particle size distribution of hard and soft wheat flour during heating. *J Cereal Sci* 40:9-16.
- Kim W and Johnson JW. 2004. The effect of rye chromatin in soft wheat. **In:** Proc 10th Internat Wheat Genet Symp (Pogna NE, Romanó M, Pogna EA, and Galterio G, Eds.). Institute Experimentale per la Cerealcoltura, Roma, Italy.
- Kim W, Johnson JW, Baenziger PS, and Gaines CS. 2004. Evaluate the effect of rye chromatin (1R) in wheat: agronomic performance. *Crop Sci* 44:1254-1258.
- Yoon S-T and Johnson JW. 2004. Microclimate, growth, and yield in wheat under north-south and east-west row orientation. *Korean J Crop Sci* 49:155-159.

**IDAHO****UNIVERSITY OF IDAHO  
Moscow and Aberdeen, ID USA.**

R. Zemetra, E. Souza, S. Guy, B. Brown, N. Bosque-Pérez, J. Hansen, K. O'Brien, M. Guttieri, D. Schotzko, T. Koehler, L. Sorensen, J. Clayton, E. Jiménez-Martínez, M. Rehman, B. Hanson, M. Kumar, D. Bowen, and A. Carter.

***Production.***

The 2004 Idaho winter wheat production was 63 million bushels, a 9 % increase from 2003. Both acreage planted and harvested decreased from the previous year but an increase in average yield to 90 bu/acre was the reason for the increase in total production. Moisture was again limiting in some areas in the late spring/summer resulting in a lower test weight in the rain-fed areas of Idaho. Stripe rust was again a problem on susceptible cultivars though infection occurred late in moderately resistant cultivars and had minimal affect on yield. Statistics for the Idaho winter wheat production for the last five years are in Table 1.

**Table 1.** Idaho winter wheat production for the last 5 years.

Year	Acres planted (x 10 <sup>3</sup> )	Acres harvested (x 10 <sup>3</sup> )	Yield (bu/acre)	Production (bu x 10 <sup>3</sup> )
2000	780	730	90	65,700
2001	760	710	73	51,830
2002	730	690	79	54,510
2003	760	720	80	57,600
2004	710	700	90	63,000

***Personnel.***

**Faculty.** Pat Shiel, University of Idaho plant virologist based on the Moscow campus, resigned to take a position in APHIS. Carl Strausbaugh, University of Idaho plant pathologist based at the Kimberly Research and Extension Center, resigned to take a position in the USDA-ARS.

**Graduate Students.** Brad Hanson completed his Ph.D. research that involved evaluating the potential for pollen-mediated gene flow among winter wheat cultivars and from wheat to jointed goatgrass. Manish Kumar completed his M.S. research on genetically modifying wheat straw to increase its potential use as a biofuel source. Arron Carter started a Masters program in the SWWW breeding program in Moscow. His two research projects involve selection of Imazamox-resistant SWWW and agronomic evaluation of a 'Coda/Brundage' RIL population.

***Cultivar development.***

**Moscow.** The SWWW cultivar **Dune** was released by the SWWW breeding program. Dune was tested in the Western Regional White Winter Wheat Nursery as 91-20503A. Dune is an early, short semidwarf wheat with excellent yield potential under both rainfed and irrigated conditions. The end-use quality of 91-20503A is good to excellent. Dune has excellent yield potential and good end-use quality.

**Aberdeen.** The southern Idaho wheat breeding program completed the release in 2004 of the HRSW **Jerome** and **Idaho 587**, a Clearfield SWSW. We are presently distributing seed of low phytic acid spring wheat lines to interested researchers under material transfer agreements. In 2005, we will propose the release of IDO597 HWSW and IDO575 HRWW. Current data summaries may be found at [www.agls.uidaho.edu/cerealsci](http://www.agls.uidaho.edu/cerealsci).

**Wheat molecular biology.**

In the wheat straw lignin-reduction project, Manish Kumar created two constructs using a portion of the CCR1 gene sequence in both sense and antisense direction to attempt to down-regulate lignin biosynthesis in wheat straw. The constructs were inserted into wheat using particle bombardment and pollen-mediated transformation. Pollen-mediated transformation was used to introduce the *bar* gene into wheat demonstrating the successful introduction of a gene into wheat by this method.

A recombinant inbred line population from the cross Coda by Brundage was created for studying traits in SWWW. Coda is an awned club wheat, and Brundage is an awnless common SWWW. The population differs for agronomic traits, disease resistance, and end-use quality. Agronomic testing of the population is currently being done in two locations as part of Arron Carter's M.S. thesis research. Seed of the 'Coda/Brundage' RIL population will be made available to interested researchers under material transfer agreements in autumn 2005.

**Biological risk assessment.**

Brad Hanson completed his research program on pollen-mediated gene flow among wheat cultivars and between wheat and jointed goatgrass. Among wheat cultivars, the maximum distance that gene flow occurred was 42 meters. Gene flow was found to be generally in the direction of the prevailing wind and occurred more often at sites with lower temperatures and higher humidity during pollination. The maximum distance for gene flow between wheat and jointed goatgrass was 40 meters from the pollen source though the frequency of 'wheat/jointed goatgrass' hybrids was much lower than that observed for gene flow among wheat cultivars.

Research continues on determining the impact of genome location on gene migration between wheat and jointed goatgrass. In the BC<sub>1</sub> generation where jointed goatgrass was the recurrent parent, retention of a herbicide resistance gene was higher than expected regardless of genome location. Based on chromosome counts it was determined that the higher than anticipated transmission rate was due to chromosome restitution and chromosome nondisjunction during gamete formation in the 'wheat/jointed goatgrass' hybrid. The BC<sub>2</sub> generation is currently under analysis to determine if genome location effect will begin to appear in the second generation of backcrossing.

**Publications.**

- Bullock DG, Bosque-Pérez NA, Johnson JB, and Merickel FW. 2004. Species composition and distribution of Hessian fly (Diptera: Cecidomyiidae) parasitoids in northern Idaho. *J Kansas Ent Soc* 77 (3):174-180.
- Castle SC, Bosque-Pérez NA, Schotzko DJ, and Guy SO. 2005. The impact of tillage practices on Hessian fly populations on fly-susceptible and resistant spring wheat varieties. *J Econ Ent* (In press).
- Clement SL, Elbertson LR, Bosque-Pérez NA, and Schotzko E. 2005. Detrimental and neutral effects of wild barley-*Neotyphodium* endophyte associations on insect survival. *Ent Exper Appl* 114 (2):119-125.
- Guttieri MJ, Bowen D, Dorsch JA, Souza E, and Raboy V. 2004. Identification and characterization of a low phytic acid wheat. *Crop Sci* 44:418-424.
- Guttieri MJ, Becker C, and Souza E. 2004. Application of wheat meal solvent retention capacity tests within soft wheat populations. *Cereal Chem* 81: 261-266.
- Hanson B. 2004. Potential for pollen-mediated gene flow among winter wheat (*Triticum aestivum*) cultivars and from wheat to jointed goatgrass (*Aegilops cylindrica*). Ph.D. Dissertation, University of Idaho, Moscow, Idaho.
- Hanson BD, Mallory-Smith CA, Shafii B, Thill DC, and Zemetra RS. 2005. Pollen-mediated gene flow from blue aleurone wheat to other wheat cultivars. *Crop Sci* (In press).
- Hanson BD, Mallory-Smith CA, Price WJ, Shafii B, Thill DC, and Zemetra RS. 2005. Interspecific hybridization: Potential for movement of herbicide resistance from wheat (*Triticum aestivum*) to jointed goatgrass (*Aegilops cylindrica*). *Weed Tech* (In press).
- Jiménez-Martínez ES and Bosque-Pérez NA. 2004. Variation in *barley yellow dwarf virus* transmission efficiency by *Rhopalosiphum padi* (Homoptera: Aphididae) after acquisition on transgenic and nontransformed wheat genotypes. *J Econ Ent* 97(6):1790-1796.
- Jiménez-Martínez ES, Bosque-Pérez NA, Berger PH, and Zemetra RS. 2004. Life history of the bird cherry-oat aphid, *Rhopalosiphum padi* (Homoptera: Aphididae) on transgenic and untransformed wheat challenged with *barley yellow dwarf virus*. *J Econ Ent* 97:203-212.

- Jiménez-Martínez ES, Bosque-Pérez NA, Berger PH, Zemetra RS, Ding H, and Eigenbrode SD. 2004. Volatile cues influence the response of *Rhopalosiphum padi* (Homoptera: Aphididae) to *barley yellow dwarf virus*-infected transgenic and untransformed wheat. *Environ Ent* 33(5):1207-1216.
- Kidwell KK, Shelton GB, DeMacon VL, Burns JW, Carter BP, Morris CF, Chen X, and Bosque-Pérez NA. 2004. Registration of 'Hollis' Wheat. *Crop Sci* 44(5):1871-1872.
- Kumar M. 2004. Genetic modification of wheat (*Triticum aestivum* L.) straw for potential use as a biofuel. Masters Thesis, University of Idaho, Moscow, Idaho.
- Rainbolt CR, Thill DC, Zemetra RS, and Shaner DL. 2005. Imidazolinone-resistant wheat acetolactate synthase (ALS) *in vivo* response to Imazamox. *Weed Sci* (In press).
- Souza EJ, Martin JM, Guttieri MJ, O'Brien K, Habernicht DK, Lanning SP, Carlson GR, and Talbert LE. 2004. Influence of genotype, environment, and nitrogen management on spring wheat quality. *Crop Sci* 44:425-432.
- Souza EJ, Guttieri MJ, and McLean R. 2004. Registration of Gary wheat. *Crop Sci* 44:1476-1477.
- Souza EJ, Guttieri MJ, and McLean R. 2004. Registration of Moreland wheat. *Crop Sci* 44:1478-1479.
- Souza EJ, Guttieri MJ, and O'Brien K. 2004. Registration of DW wheat. *Crop Sci* 44:1475-1476.
- Souza EJ, Guttieri MJ, O'Brien K, and Brown B. 2004. Registration of Alturas wheat. *Crop Sci* 44:477-1478.
- Souza EJ, Bosque-Pérez NA, Guttieri MJ, Schotzko DJ, Guy SO, Brown B, and Zemetra R. 2005. Registration of Jerome, hard red spring wheat. *Crop Sci* (In press).
- Zemetra RS, Guy SO, Lauver MA, O'Brien K, Koehler T, Robertson L, and Brown B. 2004. Registration of 'Hubbard' wheat. *Crop Sci* 44:1469-1470.
- Zhiwu L, Hansen JL, Liu Y, Zemetra RS, and Berger PH. 2004. Using real-time PCR to determine transgene copy number in wheat. *Plant Mol Biol Rep* 22:179-188.

## **INDIANA**

### **PURDUE UNIVERSITY**

**Departments of Agronomy, Entomology, and Botany and Plant Pathology, and the  
USDA-ARS Crop Production and Pest Control Research Unit, Purdue University, West  
Lafayette, IN 47907, USA.**

J.M. Anderson, S.E. Cambron, C. Crane, S.B. Goodwin, A. Johnson, J.A. Nemacheck, S. Scofield, B. Schemerhorn, R.H. Shukle, and C.E. Williams (USDA-ARS); H.W. Ohm, L. Kong, H.C. Sharma, X. Shen, and J. Uphaus (Department of Agronomy); G Buechley, D. Huber, G. Shaner, and J.R. Xu (Department of Botany and Plant Pathology); and J. Stuart (Department of Entomology).

### ***Wheat production.***

Indiana farmers harvested 178,138 ha (440,000 acres) of wheat in 2004, up 2 percent from 2003. According to the USDA National Agricultural Statistics Service, wheat yield in Indiana averaged 4,170 kg/ha (62 bu/acre) in 2004, down 6 % from the average yield in 2003. Seeding of wheat was completed generally on a timely schedule, but wet soil conditions were common especially early in the seeding season, autumn 2003. The winter was mild or there was snow cover during cold periods, resulting in little winter kill. The spring growing season was cool and wet through May, resulting in loss of nitrogen through denitrification, and accentuating effects of soil compaction from wet soil conditions at seeding in the autumn, and a resulting shallow root system especially in low-lying areas. Ample soil moisture and generally cool conditions prevailed through June, resulting in higher than typical test weight and yield of late maturing cultivars.

### ***New cultivars.***

Two new SRWWs, licensed cultivars, **INW0411** and **INW0412**, were released and seed is being increased. INW0411, tested as P97397E1-11-2-4-1-14, has low incidence and moderate type II resistance to FHB, is awnless and early like cultivar Patterson, but 4 inches shorter than Patterson, has resistance to leaf rust, powdery mildew, *Soil borne mosaic virus*, nodorum glume blotch, Septoria leaf blotch, is susceptible to Hessian fly biotype L; and has very good soft wheat milling and baking qualities. INW0412, tested as P981359C1-4-2-1-8, is early like Patterson, typically 1 to 2 inches taller than Patterson but has stronger straw, is awned, has high test weight and large kernels; has low incidence and moderate type-II resistance to FHB, nodorum glume blotch, Septoria leaf blotch, leaf rust, powdery mildew, WSBMV, is susceptible to Hessian fly biotype L, and has acceptable soft wheat milling and baking qualities.

### ***Wheat disease summary.***

Fusarium head blight, not expected to be serious due to cool conditions through mid June, developed rapidly during grain fill, and causing 5 % to 20 % estimated yield losses throughout the state. Septoria leaf blotch and nodorum blotch were present throughout Indiana and were moderately severe in the southern part of the state on susceptible cultivars. Powdery mildew was present in some areas, but not severe. Leaf rust was moderately severe on susceptible cultivars. Stripe rust occurred in some areas of the state, but was not severe.

### ***Genomics.***

**Functional analysis of genes required in disease resistance pathway of wheat (Scofield, Amanda Brandt, and Lauren Grieg).** A virus-induced gene silencing (VIGS) system has been developed for the rapid analysis of gene function in hexaploid wheat. In VIGS, viruses carrying sequences derived from plant cDNAs activate the host's sequence-specific RNA degradation system. This mechanism targets the RNAs of the viral genome for degradation, and as the virus contains transcribed plant sequence, homologous host mRNAs are also targeted for destruction, resulting in silencing the expression of the targeted gene. As the silencing mechanism is homology-dependent, it should be able to silence expression of the closely related gene present in polyploid plants. The VIGS system is based on barley stripe mosaic virus (BSMV). This virus has a tripartite single-stranded RNA genome composed of the a, b and g RNAs. Short fragments of cDNAs (150-300 bp) of wheat genes to be silenced are cloned into a DNA plasmid encoding the g RNA. *In vitro* transcribed viral RNAs are then prepared from this plasmid and those encoding the a and b genomes. These transcripts are mixed together and used to mechanically inoculate the first and second leaves of wheat seedlings. Quantitative PCR measurements of the expression of targeted genes in the third leaf (uninfected) indicate that significant suppression occurs within 5 days of viral inoculation and persists until at least 21 days after inoculation.

We are particularly interested in using VIGS to identify genes that are essential in various disease resistance pathways. Preliminary studies probing the *Lr21* leaf rust resistance pathway, in collaboration with Bikram Gill and Li Huang of Kansas State University, demonstrate that silencing *Lr21* results in conversion of resistance to susceptibility while infection with control viral constructs has no effect. We are beginning to screen for novel plant genes that encode essential functions in this resistance pathway.

**Mapping algorithms and gene expression (Charles Crane).** A polynomial-time genetic mapping algorithm was completed and tested extensively on simulated data and on real data from wheat and honeybee. Programs were also written to analyze type and frequency of repeated sequence motifs from one to 300 bases long in database-derived genomic sequence from rice, *Arabidopsis*, eight fungal genera, and in EST sequence from 55 genera of seed plants, including *Triticum*, *Aegilops*, *Hordeum*, *Secale*, *Leymus*, *Avena*, *Oryza*, *Pennisetum*, *Saccharum*, *Sorghum*, and *Zea*, among the grasses. These repeats could be simple or compound, having distinct repeated submotifs over a short span of sequence. Grasses have the most GC-rich genomes among seed plants, and this is reflected in the relative frequencies of GC-rich and AT-rich motifs. However, seed plants also vary widely in motif frequencies of similar AT content, and as might be expected, the most similar motif distributions occur in the most closely related species. Additional programs were written to relate gene expression measures between microarrays and "GeneCalling", a type of fluorescent AFLP based on cDNA obtained at different timepoints after inoculation of wheat with *Mycosphaerella graminicola*. Although problems with adaptor sequence apparently remain unresolved, the low correlation of these methods in this study falls in line with similar discrepancies in other gene-expression studies.

*Hessian fly.*

**Transcriptome analysis of the Hessian fly midgut (O. Mittapalli and R.H. Shukle).** We have undertaken an EST project on the larval Hessian fly midgut. Analysis of data sets from 1<sup>st</sup> instars and 2<sup>nd</sup> instars indicates a high proportion of full-length or near full-length cDNA clones and annotation of the assembled sequences has identified Hessian fly genes with digestion, protein metabolism, cellular communication/signal transduction, bioenergetics, detoxification/antioxidant defense, and immune responses. The annotated EST set we are developing will provide a useful resource for microarray and functional genomic studies with the Hessian fly to reveal knowledge about gene expression in the midgut at critical times in compatible and incompatible interactions with wheat. Despite its importance as a pest of wheat, knowledge of the Hessian fly and its interactions with wheat at the molecular level is limited. This research will contribute toward understanding the ability of the insect to respond to resistant wheat and the experimental dissection of the Hessian fly wheat interaction. A manuscript from this work has been accepted for publication in *Insect Molecular Biology* in 2005. A second manuscript on expression profiling of two Cytochrome P450s expressed in the larval Hessian fly midgut during compatible and incompatible interactions with wheat has been submitted to *Insect Biochemistry and Molecular Biology*.

**Population history of the Hessian fly (A.J. Johnson, B.J. Schemerhorn, and R.H. Shukle).** We have sequenced the mitochondrial 12S rRNA gene in Hessian fly populations from North America, the Mediterranean basin, and Southwest Asia. The complete complement of 12S sequences in the Hessian fly populations was subjected to a phylogenetic reconstruction. This analysis supported one of the haplotypes from the Middle East as most ancestral and revealed trends among relationships for the remaining haplotypes. To provide for a more robust phylogenetic reconstruction and analysis of population history, we are currently sequencing an 829-bp intron in a Hessian fly ortholog of the *Drosophila melanogaster white* gene for inclusion with the 12S sequences. Results to date suggest the nuclear sequence will increase the confidence values assessed by bootstrap resampling for groupings in phylogenetic trees. A manuscript from this work was published in 2004 in *The Annals of the Entomological Society of America*.

**Hessian fly resistance genes (N. Sardesai, S. Subramanyam, M.P. Giovanini, and C.E. Williams).** A new gene that confers resistance to biotype L of the Hessian fly, *H32*, was identified in the Synthetic parent of the ITMI mapping population. We scored 114 NILs from this population for resistance, and the phenotypic data were added to the marker data on the internet for mapping. The gene is located on chromosome 3DL and is flanked by an SSR that is 3.9 cM and an RFLP 3.8 cM from the gene. Linkage was confirmed by testing for cosegregation of the SSR with resistance on the 114 lines, and the map position was confirmed by using the SSR with nested deletion lines.

New wheat genes responding to feeding by first-instar Hessian fly larvae were identified. Both compatible and incompatible interactions were studied. The genes up-regulated in incompatible interactions are agglutinin isolectin (*Hfr-3*; 3,000-fold up-regulation) and flavone 3-hydroxylase. Genes up-regulated in compatible interactions are GST, connective tissue growth factor and sorbitol transporter. The gene down-regulated in incompatible interactions is a lipid transfer protein.

***H3-H6-H9-H15* linkage block (L. Kong, H.W. Ohm, S.E. Cambron, and C.E. Williams).** A sequence characterized amplified region (SCAR) marker, SOPO05<sub>909</sub>, was developed from a RAPD marker linked to gene *H9*. Linkage of the SCAR marker to *H9* was confirmed in two different F<sub>2</sub> populations. Linkage analysis identified *H9* as located near the STS marker, STS-Pm3, and eight microsatellite markers, all previously mapped to the short arm of chromosome 1A. Thus, *H9* and closely linked genes *H3*, *H6*, and *H15* are located on chromosome 1AS, contrary to their previously reported location on chromosome 5A. The locus *Xbarc263* was 1.2 cM distal to *H9* and *H9* was 1.7 cM proximal to loci *Xcfa2153*, *Xpsp2999*, and *Xgwm136*. *Xgwm136*, *Xcfa2153*, and SOPO05<sub>909</sub> were shown to be specific to *H9* and not diagnostic to several other Hessian fly-resistance genes.

*Septoria tritici blotch.*

**Mapping (S.B. Goodwin laboratory).** Testing of segregating populations to map QTL for resistance to *Septoria tritici* blotch continued in a collaborative project with Dr. Hugh Wallwork at the South Australian Research and Development Institute, Adelaide. Preliminary analyses identified possible QTL on chromosomes 3A, 3D, 4A, and 7D. Detection of

the QTL on 3A and 3D varied depending on the isolate used for inoculations, indicating some possible isolate specificity. Other testing identified a possibly new major gene for resistance in an Australian wheat cultivar and mapping of that gene continues.

Real-time PCR to estimate fungal biomass was tested as an approach to discriminate resistant and susceptible lines of wheat to *Septoria tritici* blotch. However, fungal biomass remained low even in highly susceptible plants until near the time of symptom expression, so this method may not save much time over traditional phenotypic testing and scoring of symptoms by eye. A surprising result was that fungal biomass was detected in resistant plants even 27 days after inoculation, so a resistant plant apparently does not kill the fungus. The RT-PCR approach is now being used to test whether QTL based on fungal biomass estimations are the same as those identified by phenotypic scoring.

Analyses of plant gene expression during the resistance response identified 10–50-fold increases of particular gene products occurring within a few hours after inoculation of resistant plants with the pathogen. These responses began before penetration of the host by the fungus. Additional work identified numerous genes that are expressed late during the resistance response, but only in resistant plants. Expression of these genes was much higher, from 200 to more than 1,000-fold higher, than water-inoculated controls at the same time points. Therefore, both early and late responses probably contribute to the resistance response of wheat to *Septoria tritici* blotch. Experiments with the Affymetrix Barley GeneChip Array identified numerous genes that probably are involved in the non-host resistance response of barley to the *Septoria tritici* blotch pathogen of wheat. These responses mainly involved cell wall strengthening and were different from R-gene responses seen against the closely related barley pathogen *S. passerinii* or in susceptible interactions.

**Fungal genetics (S.B. Goodwin laboratory).** A bioinformatics analysis of fungal EST sequences identified approximately 100 microsatellite-containing loci in the *Septoria tritici* blotch pathogen. Primers were designed for each locus and tested for polymorphism on a selection of field isolates plus isolates of the related fungus *S. passerinii*, the cause of speckled leaf blotch of barley. Approximately half of the primer pairs worked well and were polymorphic, and 23 of these were placed on the genetic map of the *Septoria tritici* blotch pathogen. These markers should be very useful for future studies of fungal genetics and population variability.

For more information see the Goodwin lab web site at: [http://www.btny.purdue.edu/USDA-ARS/Goodwin\\_lab/Goodwin\\_Lab.html](http://www.btny.purdue.edu/USDA-ARS/Goodwin_lab/Goodwin_Lab.html).

### ***Yellow dwarf viruses.***

**Resistance (H. Wiangjun and J.M. Anderson).** Previous data has resulted in three possible models for the mechanism of intermediate wheatgrass (*Th. intermedium*)-derived CYDV resistance (Wiangjun and Anderson 2003, Phytopath 94:1102-1106). This resistance has been given the gene name of *Bdv3*. Further study has shown that while CYDV replication can occur in non-vascular and vascular tissue in resistant and susceptible wheat lines cellular analyses have demonstrated that the most likely mechanism is an inhibition of long-distance transport. CYDV can spread from the infected companion cells into adjacent sieve elements but its movement beyond this point is blocked. These analyses have also shown that the feeding behavior of the aphid is affected in the resistant line. The aphid deposits virus more often in non-vascular cells in the resistant line compare with the susceptible line suggesting that the aphid needs to probe more before it finds the vascular tissue.

**Gene expression analysis (B. Balaji and J.M. Anderson).** Over 200 genes whose expression changes in YDV resistant and susceptible lines after YDV infection were identified using Suppressive Subtractive Hybridization (SSH) Quantitative Real time-PCR (Q-RT-PCR) has been used to verify that these are differentially expression. To facilitate these studies it was necessary to choose the appropriate endogenous control genes as internal references in Q-RT-PCR. Two classes of genes were found that could be used as controls for genes that accumulate high levels of transcripts with abundant messages (28S and 18S rRNA) and low amount of transcripts (GAPDH, rbcL). These studies also showed that ubiquitin and rbcS were not useful endogenous control genes as their expression was not constant in our resistant and susceptible lines with or without virus infection.

**Wheatgrass molecular markers (Platteter, Mullen, Francki, and J.M. Anderson).** Utilizing the data derived from the NSF funded wheat ESTs bin-mapping project as a resource those ESTs which had microsatellite sequences within

them were examined to identify dominant or codominant wheatgrass/wheat SSR markers for integrating biotic or abiotic resistance genes into wheat. Using addition and substitution lines containing *Lophopyrum elongatum* chromosomes several SSR markers were found for each *Lophopyrum* chromosome except 4E. The proportion of polymorphic markers was greater when the primer containing regions flanking the SSR were highly conserved between two species such as wheat, barley, rice, and oat. Additional work has identified more wheat ESTs that produced SSR markers for the *L. elongatum* 1E, 2E, and 7E chromosomes.

**Wheat-*Thinopyrum* mosaic chromosomes (L. Ayala, N. Thompson, and J.M. Anderson).** The PCR markers described above and other PCR markers were used to increase the resolution of the RFLP-based map from *Th. intermedium*/wheat  $M_4$  recombinant lines (Crasta et al. 2000, Genome 43:698-706) we added PCR-derived markers. Fluorescent *in situ* hybridization using GISH and repetitive (FISH) DNA probes also were used to physically analyses the lines. The  $F_2$  progeny of two  $M_4$  lines crossed to Chinese Spring were examined with the PCR markers for the presence of *Th. intermedium* segregating fragments. These data showed that significantly more recombination had occurred in these lines then previously thought, given the analysis of these chromosomes in the  $M_4$  generation because in most of the  $F_2$  recombinant lines tested, the chromosome 7D/7E appeared to be a mosaic of wheat and *Th. intermedium* chromatin sections. These observation contrasts with most of the literature which suggests that recombination between homeologous chromosomes from different genomes have very low rates of recombination. Our data suggest that introgressing the many agronomically useful traits in *Th. intermedium* or other related wheatgrass species into wheat may be much more feasible then previous thought.

**7E translocations (H.C. Sharma, X. Shen, and H.W. Ohm).** The process of shortening the 7E chromosome segment in P961341 and KS24-2-11 continued. P961341 is a translocation with yellow dwarf viruses resistance from *Th. intermedium* and KS24-2-11 is a translocation with FHB resistance from *Lophopyrum (Thinopyrum) ponticum*.  $F_4$  populations from 'P961341/*ph1ph1*' and 'KS24-2-11/*ph1ph1*' crosses were characterized to isolate potential recombinants.

Alien addition lines of *A. cristatum* in wheat, received from J. Jahier, France, were tested for winter hardiness in Indiana during the 2003–04 wheat season. No winter hardiness was found in these lines.

### Research personnel.

Tika Adhikari, postdoctoral associate with Steve Goodwin, accepted a position as assistant professor in the Department of Plant Pathology at North Dakota State University, where he will continue to work on cereal diseases. Jessy Gilsinger completed M.S. degree requirements under the guidance of Herb Ohm and is studying for a Ph.D. at North Carolina State University in soybean genetics/breeding under the guidance of Dr. Joseph Burton. Ligia Ayala, postdoctoral associate with Joe Anderson, accepted a postdoctoral position at CSIRO in Canberra Australia with Phil Larkin where she will continue to work on YDV and other cereal diseases. Boovaraghan Balaji, postdoctoral associate with Joe Anderson, accepted a postdoctoral position in the Plant Pathology Department at the University of Missouri examining differential gene expression following virus infection in *Nicotiana*. Nicole Thompson, postdoctoral associate with Joe Anderson, accepted a postdoctoral position at Adelaide University working on Mundulla Yellows, a disease affecting eucalyptus.

### Publications.

- Adhikari TB, Balaji B, Breeden J, Anderson JM, and Goodwin SB. 2004. Quantification of *Mycosphaerella graminicola* in wheat by real-time PCR. *Phytopath* 94:S2.
- Adhikari TB, Balaji B, Breeden J, Crane C, Anderson JM, and Goodwin SB. 2004. Real-time PCR analysis of genes expressed during wheat-*Mycosphaerella graminicola* interactions. *Phytopathology* 94:S3.
- Adhikari TB, Wallwork H, and Goodwin SB. 2004. Microsatellite markers linked to the *Stb2* and *Stb3* genes for resistance to Septoria tritici blotch in wheat. *Crop Sci* 44:1403-1411.
- Adhikari TB, Cavaletto JR, Dubcovsky J, Gieco J, Schlatter AR, and Goodwin SB. 2004. Molecular mapping of the *Stb4* gene for resistance to Septoria tritici blotch in wheat. *Phytopathology* 94:1198-1206.
- Adhikari TB, Cavaletto JR, Hu X, Shaner G, and Goodwin SB. 2004. Molecular mapping of the Septoria tritici blotch resistance gene *Stb1* in wheat. *Plant and Animal Genome XII*, P454. ([http://www.intl-pag.org/12/abstracts/P5c\\_PAG12\\_454.html](http://www.intl-pag.org/12/abstracts/P5c_PAG12_454.html)).

- Adhikari TB, Yang X, Cavaletto JR, Hu X, Buechley G, Ohm HW, Shaner G, and Goodwin SB. 2004. Molecular mapping of *Stb1*, a potentially durable gene for resistance to Septoria tritici blotch in wheat. *Theor Appl Genet* 109:944-953.
- Anderson JM. 2004. Analysis of the wheat defense-response transcriptome using an unbiased, open-architecture gene-identification system combined with microarrays. **In:** International Triticeae Mapping Initiative Summer Workshop. Minneapolis, MN. p.13.
- Anderson JM, Balaji B, and Ohm HW. 2004. Analysis of resistance and susceptibility to barley and cereal yellow dwarf virus. **In:** Proc 7th Internat Oat Conf, Helsinki, Finland.
- Balaji B, Thompson N, and Anderson JM. 2004. Real-time quantitative PCR of wheatgrass-specific markers to confirm alien translocation and BYDV/CYDV resistance in wheat. *Phytopath* 94:S6.
- Balaji B and Anderson JM. 2004. Choosing appropriate endogenous control genes as internal references for quantitative real-time PCR analysis in cereals crops. *Exp Bot* (In press).
- Behura SK, Valicente FH, Rider SD Jr, Chen MS, Jackson S, and Stuart JJ. 2004. A physically anchored genetic map and linkage to avirulence reveals recombination suppression over the proximal region of Hessian fly chromosome A2. *Genetics* 167:343-355.
- Boukar O, Kong L, Singh BB, Murdock L, and Ohm HW. 2004. AFLP and AFLP-derived SCAR markers associated with *Striga gesnerioides* resistance in cowpea. *Crop Sci* 44:1259-1264.
- Carvalho CHS, Zehr UB, Gunaratna N, Anderson JM, Kononowicz HH, Hodges TK, and Axtell JD. 2004. *Agrobacterium*-mediated transformation of sorghum: factors that affect transformation efficiency. *Genet Mol Biol* 27:259-269.
- Crane CF and Crane YM. 2004. A nearest-neighboring-ends algorithm for genetic mapping. *Bioinformatics* (<http://bioinformatics.oupjournals.org/cgi/content/abstract/bti164> from 24 November 2004).
- Crane CF and Crane YM. 2004. Flipper: A general, high-capacity genetic mapping program. *Plant and Animal Genome XII*, C993.
- Crane CF and Crane YM. 2004. A nearest-neighboring-ends algorithm for genetic mapping. *Plant and Animal Genome XII*, P976.
- Crane CF. 2004. A genetic map of the ITMI population using the nearest-neighboring-ends algorithm. *International Triticeae Mapping Initiative Summer Workshop*, St. Paul, MN.
- El Khelifi O, Sharma H, Malki M, and Benlhabib O. 2004. Transfer a des Bles marocains, a la suite de croisement avec *Aegilops squarrosa*, de genes de resistance a la mouche de Hesse. *Acta Bot Gallica* 150:127-135 (In French).
- El Khelifi O, Sharma H, Chamlal H, and Benlhabib O. 2004. Introgression de la resistance a la cecidomyie chez Ble par croisement avec une souche d' *Aegilops ventricosa* marocaine. *Acta Bot Gallica* 150:411-419 (In French).
- El Khelifi O, Chamlal H, Sharma H, and Benlhabib O. 2004. Interspecific cross between durum wheat and *Aegilops geniculata* to transfer resistance to Hessian fly. *Acta Bot Malacitana* 28:149-154.
- Goodwin SB. 2004. Minimum phylogenetic coverage: an additional criterion to guide the selection of microbial pathogens for initial genomic sequencing efforts. *Phytopath* 94:800-804.
- Goodwin SB, Cavaletto JR, van der Lee T, Lintel HB, and Kema GHJ. 2004. Mining microsatellites in an EST database of *Mycosphaerella graminicola*. **In:** Proc 7th Eur Conf Fungal Genetics, Copenhagen, Denmark. P. 223.
- Goodwin SB, Waalwijk C, and Kema GHJ. 2004. Genetics and genomics of *Mycosphaerella graminicola*: a model for the Dothideales. **In:** Applied Mycology and Biotechnology. Vol 4. Fungal Genomics (Arora DK and Khachatourians GG, Eds.). Elsevier B.V., Amsterdam. Pp. 315-330.
- Kong L, Anderson JM, and Ohm HW. 2004. Identification and characterization of defense response genes from wheat differentially induced by infection with *Fusarium graminearum*. *Plant and Animal Genome XII*, P156.
- Johnson AJ, Schemerhorn BJ, and Shukle RH. 2004. A first assessment of mitochondrial DNA variation and geographic distribution of haplotypes in the Hessian fly (*Diptera: Cecidomyiidae*). *Ann Ent Soc Amer* 97(5): 940-948.
- Kong L, Anderson JM, and Ohm HW. 2005. Induction of wheat defense and stress-related genes in response to *Fusarium graminearum*. *Genome* (In press).
- Kong L, Anderson JM, and Ohm HW. 2004. Identification and characterization of defense response genes from wheat differentially induced by infection with *Fusarium graminearum*. *PAG XII*, P156.
- Miller WA, Anderson JM, Gray SM, Gai X, and Beckett R. 2004. Global BYDV/CYDV sequencing project. *Phytopath* 94:S71.
- Mittapalli O, Neal JJ, and Shukle RH. 2005. Differential expression of two cytochrome P450 genes in compatible and incompatible Hessian fly/wheat interactions. *Insect Biochem Mol Biol* (In press).
- Mittapalli O, Stuart JJ, and Shukle RH. 2005. Molecular cloning and characterization of two digestive serine proteases from the Hessian fly, *Mayetiola destructor*. *Insect Mol Biol* (In press).

- Ohm HW, Anderson JM, Sharma HC, Ayala L, Thompson N, and Uphaus JJ. 2005. Registration of yellow dwarf viruses resistant wheat germplasm line P961341. *Crop Sci* 45:805-806.
- Ohm HW, Patterson FL, Ratcliffe RH, Cambron SE, and Williams CE. 2004. Registration of Hessian fly resistant wheat germplasm line P921696. *Crop Sci* 44:2272-2273.
- Pitt WM, Goodwin SB, Ash GJ, Cother NJ, and Cother EJ. 2004. *Plectosporium alismatis* comb. nov., a new placement for the *Alismataceae* pathogen *Rhynchosporium alismatis*. *Mycol Res* 108:775-780.
- Puthoff DP, Nemacheck JA, and Williams CE. 2004. *Hfr-2*, a Hessian fly-responsive gene from wheat, has similarity to a seed storage protein, a lectin and a bacterial toxin protein.. *Plant and Animal Genome XII*, P462.
- Scofield SR, Brandt AS, Anderson JM, Crane C, Goodwin SB, Ohm HW, Williams CE, Lohret T, and Crasta OR. 2004. Functional pathogenomics in cereals. *Plant and Animal Genome XII*, P839.
- Sharkhuu A, Goldsbrough PB, Goodwin SB, and Weller SC. 2004. RAPD analysis on genetic diversity of nightshade species in the north central region. North Central Weed Science meetings.
- Sharma HC. 2004. Embryo rescue in wide crosses: review. **In:** *Recent Res Dev Genet Plant Breed* 1:287-308. Research Sign Post.
- Sharma HC, Ohm H, and Shaner G. 2004. Resistance to barley yellow dwarf virus, powdery mildew and leaf rust in wheat x *Thinopyrum* backcrosses. *Phytoprotection* 85:27-32.
- Sharma HC, Ohm H, and Shaner G. 2004. Resistance to yellow dwarf virus, powdery mildew and leaf rust in wheat x *Thinopyrum intermedium* backcrosses. *Agron Abst*:96.
- Shen X, Kong L, Sharma H, and Ohm H. 2004. Marker-assisted characterization of FHB resistance in *Lophopyrum*-derived wheat lines. **In:** *Proc 2nd Internat Fusarium Conf*, Orlando, FL, 11-16 December.
- Shen X, Kong L, and Ohm H. 2004. Fusarium head blight resistance in hexaploid wheat (*Triticum aestivum*)-*Lophopyrum* genetic lines and tagging of the alien chromatin by PCR markers. *Theor Appl Genet* 108:808-813.
- Shen X, Kong L, and Ohm H. 2004. Marker-assisted characterization of Fusarium head blight resistance in wheat derived from wheatgrass. *Plant and Animal Genome XII*, P451.
- Soria MA, Khan IA, Anderson JA, Brown-Guedira G, Campbell KG, Elias EM, Fritz AK, Gill BS, Gill KS, Haley S, Kianian SF, Kidwell K, Lapitan NLV, Ohm H, Sherman JD, Sorrells ME, Souza E, Talbert L, and Dubcovsky J. 2004. The MAS wheat project: Bringing Genomics to the Wheat Fields. *Plant and Animal Genome XII*, P216.
- Subramanyam S, Sardesai N, and Williams CE. 2004. Expression of two defense-responsive genes, *Hfr-1* and *WCI-1* under biotic and abiotic stress. *Plant and Animal Genome XII*, P902.
- Thompson N and Anderson JM. 2004. Analysis of a repeat sequence pAW161 in wild wheatgrass accessions. **In:** *International Triticeae Mapping Initiative Summer Workshop*. Minneapolis, MN. p.52.
- Thompson N, Ayala L, and Anderson JM. 2004. Molecular markers for a *Thinopyrum intermedium* translocation carrying resistance to YDV into wheat and validation by FISH. **In:** *Plant and Animal Genome XII*, P324.
- Ware SB, Verstappen ECP, Cavaletto JR, Goodwin SB, Waalwijk C, and Kema GHJ. 2004. Identification of the teleomorph of *Septoria passerinii*, the barley speckled leaf pathogen. **In:** *Proc 7th Eur Conf Fungal Genet*, Copenhagen, Denmark, p. 94.
- Wiangjun H and Anderson JM. 2004. The basis for *Thinopyrum*-derived resistance to *Cereal yellow dwarf virus*. *Phytopath* 94:1102-1106.
- Wiangjun H and Anderson JM. 2004. Wheatgrass-Derived Resistance Inhibits Movement of *Cereal Yellow Dwarf Virus* within the Sieve Tubes. **In:** *Proc Midwest ASPB Sectional Meeting and Plant Molecular Biology and Biotechnology Symposium* p. 37.
- Yoshiyama M and Shukle RH. 2004. Molecular cloning and characterization of a glutathione S-transferase gene from Hessian fly (Diptera: Cecidomyiidae). *Ann Entomol Soc Amer* 97(6):1285-1293.

**KANSAS****KANSAS AGRICULTURAL STATISTICS****Room 200, 632 S.W. van Buren, P.O. Box 3534, Topeka, KS 66601-3534, USA.*****Jagger still most popular.***

Jagger was the leading cultivar of wheat seeded in Kansas for the 2005 crop. Accounting for 28.2 percent of the state's wheat. Jagger decreased 12.7 points from a year ago but was the most popular cultivar in six of the nine districts.

Jagalene moved up to second place with 21.2 percent of the acreage. Jagalene increased 18.2 points and ranked in the top five for all nine districts.

The KSU-maintained cultivar 2137 came in third, down 2.9 points from last year. TAM 110 moved down to fourth place with 3.3 percent of the acreage. The OSU-maintained cultivar 2174 moved up to fifth place with 3.0 percent of the state's acreage. Trego, a hard white wheat, fell to sixth place with 2.9 percent. The KSU-maintained cultivar 2145 and Overley were both new to the top ten and tied for seventh place with 2.2 percent. Cutter and Thunderbolt also were both new to the top ten and tied for ninth place with 1.7 percent. Acres planted with blended cultivars were not included in the rankings by cultivar. Blends accounted for 11.3 percent of the state's planted acres and were used more extensively in the north-central, northeast, and central areas. Out of the total acres planted with blends, 73.5 percent included Jagger in the blend, and 41.2 percent had 2137. Hard white cultivars accounted for 3.9 percent of the state's acreage. Trego was the leading hard white cultivar, accounting for 74.0 percent of the state's white wheat. The majority of the white wheat was planted in the western third of the state. This wheat cultivar project is funded by the Kansas Wheat Commission.

**Table 1.** Top 10 wheat cultivars grown in the state of Kansas for the 2005 crop and percent of seeded acreage.

1. Jagger	28.2	6. Trego	2.9
2. Jagalene	21.2	7. 2145	2.2
3. 2137	5.7	Overley	2.2
4. TAM 110	3.3	8. Cutter	1.7
5. 2174	3.0	Thunderbolt	1.7

**Table 2.** Top wheat cultivars planted in Kansas by district and percent of seeded acreage in 2005.

<b>DISTRICT 10 (NORTHWEST)</b>		<b>DISTRICT 40 (NORTH CENTRAL)</b>		<b>DISTRICT 70 (NORTHEAST)</b>	
Jagger	25.6	Jagger	20.7	2137	16.0
Jagalene	15.1	Jagalene	19.5	Jagger	14.7
2137	8.2	2145	9.7	2145	13.4
Trego-HWWW	7.5	2137	7.1	Jagalene	12.6
Thunderbolt	5.0	Karl/Karl 92	5.0	Karl/Karl 92	8.1
<b>DISTRICT 20 (WEST CENTRAL)</b>		<b>DISTRICT 50 (CENTRAL)</b>		<b>DISTRICT 80 (EAST CENTRAL)</b>	
Jagalene	13.3	Jagalene	28.8	Jagger	32.2
TAM 110	12.4	Jagger	27.1	2137	16.5
Jagger	10.8	2137	7.3	Jagalene	14.5
Trego-HWWW	10.7	Cutter	3.6	Dominator	8.4
T81	6.7	Overley	3.3	2145	5.1
<b>DISTRICT 30 (SOUTHWEST)</b>		<b>DISTRICT 60 (SOUTH CENTRAL)</b>		<b>DISTRICT 90 (SOUTHEAST)</b>	
Jagger	23.1	Jagger	40.8	Jagger	23.8
Jagalene	15.8	Jagalene	25.0	2137	19.7
TAM 110	15.4	2174	8.0	Jagalene	17.4
2137	6.6	Overley	4.2	2174	9.8
Ike	5.7	2137	3.3	Onago	7.3

**Table 3.** Distribution of Kansas winter wheat cultivars, 2004 crop (— = cultivar not reported in this district; 0 = < 1 %).

Cultivar	Agricultural Statistics Districts									
	NW	WC	SW	NC	C	SC	NE	EC	SE	State
	percent of seeded acreage									
Jagger	25.6	10.8	23.1	20.7	27.1	40.6	14.7	32.2	23.8	28.2
Jagalene	15.1	13.3	15.8	19.5	28.8	25.0	12.6	14.5	17.4	21.2
2137	8.2	6.4	3.9	7.1	7.3	3.3	16.0	16.5	19.7	5.7
TAM 110	1.5	12.4	15.4	—	0.3	0.2	—	—	—	3.3
2174	—	—	0.2	0.0	1.6	8.0	—	5.1	9.8	3.0
Trego-HWWW	7.5	10.7	6.6	0.3	0.8	0.1	—	—	—	2.9
2145	0.0	0.2	—	9.7	1.8	0.6	13.4	5.0	2.8	2.2
Overley	0.1	0.1	0.1	1.1	3.3	4.2	3.0	3.8	4.1	2.2
Cutter	0.2	1.1	0.2	1.2	3.6	2.5	—	—	0.0	1.7
Thunderbolt	5.0	3.9	3.6	0.3	0.9	0.4	—	—	—	1.7
T81	0.5	6.7	4.9	1.8	0.0	0.1	—	—	—	1.6
Karl/Karl 92	0.6	1.5	0.0	5.0	1.7	0.3	8.1	1.9	1.6	1.5
Stanton	3.9	5.0	4.2	—	0.0	0.0	—	—	—	1.4
Ike	1.9	3.3	5.7	0.1	0.9	0.2	—	—	—	1.4
Dominator	0.1	—	—	3.6	2.8	0.1	6.0	8.4	—	1.1
TAM 107	3.0	4.1	2.1	—	0.2	—	—	—	—	1.0
Akron	0.4	4.0	0.1	—	—	—	—	—	—	0.5
Coronado	—	0.1	—	—	0.3	1.0	—	—	—	0.4
NuHills-HWWW	1.3	0.4	0.9	—	—	0.1	—	—	—	0.3
Larned	0.4	1.0	1.3	0.1	0.1	—	—	—	1.5	0.3
Custer	—	—	0.1	—	—	0.9	—	—	—	0.3
Vista	1.9	0.6	—	—	—	—	—	—	—	0.3
TAM 111	0.3	1.3	0.4	0.0	—	—	—	—	—	0.2
Dumas	0.5	—	1.0	—	—	—	—	—	—	0.2
NuFrontier-HWWW	1.7	0.3	0.3	—	—	0.0	—	—	—	0.2
2163	—	—	0.2	0.1	0.3	0.3	0.1	5.0	2.9	0.2
Venango	—	—	—	—	0.2	0.4	0.7	—	—	0.2
Blends	9.9	4.8	3.4	26.9	14.9	7.1	17.8	3.6	3.9	11.3
Other HWWW Cultivars	0.5	1.0	1.9	—	0.2	0.1	—	—	—	0.5
Other Hard Cultivars	8.8	6.9	4.0	2.5	2.9	4.4	7.6	3.4	10.8	4.8
Other Soft Cultivars	—	—	0.0	—	—	—	—	0.6	1.5	0.0
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

**Table 4.** Distribution of Kansas winter wheat cultivars, specified years.

	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005
Cultivar	percent of seeded acreage									
Jagger	1.0	6.4	20.2	29.2	34.0	35.8	42.8	45.2	40.9	28.2
Jagalene	—	—	—	—	—	—	—	—	3.0	21.2
2137	—	1.0	13.5	22.0	23.1	22.3	15.5	13.3	8.6	5.7
TAM 110	—	—	—	0.5	1.3	2.8	3.0	3.8	4.2	3.3
2174	—	—	—	—	1.1	3.0	3.1	3.1	2.8	3.0
Trigo-HWWW	—	—	—	—	—	0.3	0.8	1.8	3.5	2.9
2145	—	—	—	—	—	—	—	—	1.5	2.2
Overley	—	—	—	—	—	—	—	—	0.1	2.2
Cutter	—	—	—	—	—	—	—	—	0.7	1.7
Thunderbolt	—	—	—	—	—	0.2	0.6	0.8	1.4	1.7
T81	—	—	—	—	0.2	0.2	0.8	0.6	1.8	1.6
Karl/Karl 92	20.9	22.1	10.8	5.9	3.5	3.3	3.6	3.2	2.3	1.5
Stanton	—	—	—	—	—	—	0.1	0.6	1.4	1.4
Ike	7.2	10.5	7.0	5.5	4.1	3.6	2.6	2.1	2.0	1.4
Dominator	—	—	0.2	0.8	1.4	1.5	2.0	2.2	1.5	1.1
TAM 107	17.1	17.0	12.6	8.3	6.3	5.3	2.9	2.3	1.3	1.0
Akron	—	—	0.4	0.8	1.0	0.4	0.4	0.2	0.9	0.5
Coronado	—	—	0.8	1.3	1.0	1.1	0.7	0.8	0.5	0.4
NuHills-HWWW	—	—	—	—	—	—	—	—	—	0.3
Larned	4.8	3.6	2.4	1.9	1.2	1.0	0.9	0.8	0.4	0.3
Vista	0.8	1.2	1.1	0.9	0.9	1.0	0.9	0.3	0.2	0.3
TAM 111	—	—	—	—	—	—	—	—	—	0.2
Dumas	—	—	—	—	—	—	—	—	0.1	0.2
NuFrontier-HWWW	—	—	—	—	—	—	0.1	0.3	0.6	0.2
Longhorn	0.5	0.3	0.2	0.1	0.2	0.1	0.2	0.1	0.1	0.2
2163	19.8	15.4	10.4	3.4	2.3	2.0	1.3	0.8	0.3	0.2
Vennago	—	—	—	—	—	—	0.1	0.1	0.2	0.2
Blends	—	—	2.6	6.1	7.5	7.0	11.4	12.8	15.2	11.3
Other HWWW Cultivars	—	—	—	—	0.2	0.8	0.3	0.2	0.1	0.5
Other Hard Cultivars	12.7	10.3	9.0	7.0	4.7	3.8	8.3	3.0	2.5	4.8
Other Soft Cultivars	—	—	—	0.0	2.0	0.0	0.1	0.1	0.0	0.0
Total	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0

**KANSAS STATE UNIVERSITY**

**Environmental Physics Group, Department of Agronomy, Kansas State University,  
Throckmorton Hall, Manhattan, KS 66506-5501, USA.**

**News.**

M.B. Kirkham is on sabbatical leave with Dr. Brent E. Clothier at the Horticultural and Food Research Institute of New Zealand, Ltd. in Palmerston North between 14 January and 14 April, 2005. Methods to control nitrogen losses from grazed pastures are being studied including inhibitors added directly to urine patches, where most of the nitrogen is concentrated.

James Kingston (Ken) McCarron continues as visiting scholar in the group.

Dr. Kirkham's book has been published. *Principles of Soil and Plant Water Relations*, M.B. Kirkham. 2005. Elsevier Academic Press, San Diego. xvii + 500 pages. ISBN: 0-12-409751-0. Web page for book: [http://www.elsevier.com/wps/find/bookdescription.cws\\_home/703882/description](http://www.elsevier.com/wps/find/bookdescription.cws_home/703882/description). The book has a chapter on agronomic applications of Poiseuille's law using wheat roots. For a complete description of this book, see p. 14 of the volume.

**Publications.**

- de Willigen P, Heinen M, and Kirkham MB. 2005. Transpiration and root water uptake. **In:** Encyclopedia of Hydrological Sciences. John Wiley and Sons, London (In press).
- Kirkham MB. 2004. Water-use efficiency. **In:** Encyclopedia of soils in the environment (Hillel E Ed). Elsevier Academic Press, San Diego, CA. Pp. 315-322.
- Liphadzi MS and Kirkham MB. 2005. Phytoremediation of soil contaminated with heavy metals: A technology for rehabilitation of the environment. *S Afr J Bot* (In press).
- Liphadzi MS and Kirkham MB. 2005. Heavy metal toxicity: physiological and cellular processes. **In:** Plant-Environment Interactions (Huang B Ed). CRC Press, Boca Raton, FL (In press).
- Madrid F and Kirkham MB. 2005. Testing the manipulation of soil availability of metals. **In:** Phytoremediation (Willey N Ed). Humana Press, New Jersey (In press).
- Nagaraj N, Reese JC, Tuinstra MR, Smith CM, St. Amand P, Kirkham MB, Kofoed KD, Campbell LR, and Wilde GE. 2005. Molecular mapping of sorghum genes expressing tolerance to damage by the greenbug (Homoptera: Aphididae). *J Environ Ent* (In press).
- van der Ploeg RR, Böhm W, and Kirkham MB. 2004. Liebig, Justus Von. **In:** Encyclopedia of soils in the environment (Hillel E Ed). Elsevier Academic Press, San Diego, CA. Pp. 343-349.
- Welch SM, Roe JL, Das S, Dong Z, He R, and Kirkham MB. 2005. Merging genomic control networks and soil-plant-atmosphere-continuum (SPAC) models. *Agric Systems* (In press).
- Woche SK, Goebel MO, Kirkham MB, Horton R, van der Ploeg RR, and Bachmann J. 2005. Contact angle of soils as affected by depth, texture, and land management. *Eur J Soil Sci* (In press).

**THE WHEAT GENETICS RESOURCE CENTER AND THE USDA-ARS**

**Department of Plant Pathology, Throckmorton Hall, Manhattan, KS 66506-5502, USA.  
<http://www.ksu.edu/wgrc>**

**Notice of release of KS04WGRC45 leaf rust-resistant hard white winter wheat germ plasm.**

B. Friebe, D.L. Wilson, W.J. Raupp, and B.S. Gill, and G.L. Brown-Guedira (USDA-ARS).

KS04WGRC45 hard white winter wheat germ plasm is homogeneous for resistance to leaf rust at the seedling and adult plant stages. KS04WGRC45 is an F<sub>3</sub>-derived line from the cross 'Heyne\*2//TA5586 (Chinese Spring-mono1B/CS DA

*Elymus trachycaulus* 1H<sup>i</sup>). Leaf rust resistance of the germ plasm is derived from *Elymus trachycaulus* (Link) Gould ex Shinnery accession (TA12052). Chromosome 1H<sup>i</sup> was transferred from TA12052 to Chinese Spring wheat during the production of a set of wheat-*E. trachycaulus* chromosome addition lines. The Robertsonian translocation T1H'S-1BL consisting of the short arm of the *E. trachycaulus* chromosome 1H<sup>i</sup> translocated to the long arm of wheat chromosome 1B was recovered in the offspring of a plant double monosomic for chromosomes 1H<sup>i</sup> and 1B. This translocation stock, designated TA5586, was crossed twice to the HWWW cultivar Heyne. The BC<sub>1</sub> and BC<sub>2</sub> progeny were screened for their reaction to leaf rust with race PBJL, which is virulent on the recurrent parent Heyne (infection type (IT) = 4, large uredinia, lacking chlorosis or necrosis). The BC<sub>2</sub>F<sub>2</sub> families derived from resistant plants were again screened for leaf rust resistance and one family was selected with IT = 2 (small to moderate size uredinia with chlorosis). The 12 BC<sub>2</sub>F<sub>3</sub> lines derived from this family were analyzed by GISH, and one line homozygous for the translocation chromosome T1H'S-1BL was selected as KS04WGRC45.

When evaluated in the field under heavy inoculum pressure at Manhattan, KS in the 2003–04 growing season, a trace of leaf rust was detected on adult plants of KS04WGRC45. The recurrent parent Heyne had a susceptible reaction covering approximately 30 % of the leaf area. Intermediate infection types (IT = 2+, moderate size uredinia with chlorosis) were observed on seedlings of KS04WGRC45 and TA5586 when evaluated with *P. tritricina* races MCRL and TNRJ and a collection from the field in Manhattan, KS, in 2003. High infection types of 3–4 (moderate to large uredinia, lacking chlorosis or necrosis) were observed on seedlings of Heyne and Chinese Spring with all the races of leaf rust tested.

### ***Notice of release of KS04WGRC46 Fusarium head blight-resistant hard red winter wheat germ plasm.***

G.L. Brown-Guedira (USDA-ARS); W.W. Bockus, M.A. Davis, and B.S. Gill (Department of Plant Pathology); D.A. Van Sanford (Department of Agronomy, University of Kentucky, Lexington, KY); and J.P. Murphy (Department of Crop Science, North Carolina State University, Raleigh, NC).

KS04WGRC46 is a BC<sub>2</sub>F<sub>5</sub>-derived hard red winter wheat line from the cross 'Wrangler\*3/TA960'. Fusarium head blight resistance of the germ plasm is derived from accession TA960 of *T. timopheevii* subsp. *armeniacum*. Significantly less disease was observed on plants of KS04WGRC46 in growth chamber tests with point inoculations of *F. graminearum* than on the recurrent parent, indicating that KS04WGRC46 has type-II resistance to FHB. A mean of 11.18 % infected spikelets was observed on KS04WGRC46 and the recurrent parent Wrangler had a mean of 38.17 % infected spikelets. Mean disease severity on the resistant and susceptible check cultivars Sumai 3 and Trego were 7.5 and 70.0 % infected spikelets, respectively (LSD = 19.8, P = 0.05). When KS04WGRC46 was evaluated in inoculated field nurseries at Manhattan, KS, in the 2001 and 2003 growing seasons, 11.7 and 5.7 % of spikelets, respectively, had symptoms of FHB infection. These levels were significantly less than those observed on the winter wheat cultivars 2137 (susceptible, 48.2 and 45.0 % infected spikelets in 2001 and 2003, respectively) and Karl 92 (intermediate, 37.4 and 25.6 % infected spikelets in 2001 and 2003, respectively). The resistant hard winter wheat cultivar Heyne had 15.2 and 11.5 % infected spikelets in 2001 and 2003, respectively. Inheritance of resistance to FHB in KS04WGRC46 is not known.

### ***Notice of release of KS04WGRC47 leaf rust-resistant hard red winter wheat germ plasm.***

G.L. Brown-Guedira (USDA-ARS); A.K. Fritz (Department of Agronomy); B.S. Gill; and T.S. Cox (Land Institute, Salina, KS).

KS04WGRC47 is a BC<sub>3</sub>F<sub>5</sub>-derived line with the pedigree 'Karl 92'\*4/TA1836'. Karl 92 is a HRWW cultivar, and TA1836 is a leaf rust-resistant accession of *Ae. speltoides*. Seedlings of KS04WGRC47 exhibited a low infection type (IT = 0; to ;1, small flecks or small pustules with chlorosis) when inoculated races KDBL, PNMQ, MCDL, MFBL, and TNRJ of *P. tritricina*. Moderate to high infection types (IT = 2 to 4, moderate to large pustules with little or no chlorosis) were observed on seedlings of Karl 92 with all races of leaf rust tested. Adult plants of KS04WGRC47 displayed a low infection type (;) when exposed to moderate to heavy leaf rust inoculum levels in the field at Manhattan and Hutchinson, Kansas in 2002, 2003, and 2004, and under heavy inoculum pressure at Castroville, TX, in 2004. Except for resistance to leaf rust, KS04WGRC47 is similar to Karl 92 in height, heading date, and overall phenotype.

Leaf rust resistance in KS04WGRC47 is due to a single dominant gene from TA1836. The relationship of the leaf rust resistance gene in KS04WGRC47 with the *Ae. speltoides* derived leaf rust resistance genes, *Lr28*, *Lr36*, *Lr47* and *Lr51* is not known.

### ***Notice of release of KS04WGRC48 hard red winter wheat germ plasm resistant to leaf rust and powdery mildew.***

G.L. Brown-Guedira (USDA-ARS); T.S. Cox (Land Institute, Salina, KS); P. D. Chen (Cytogenetics Institute, Nanjing Agricultural University, Nanjing, Jiangsu, P.R. China); D.A. Van Sanford (Department of Agronomy, University of Kentucky, Lexington, KY); A.K. Fritz (Department of Agronomy, Kansas State University); and B.S. Gill.

KS04WGRC48 is a BC<sub>1</sub>F<sub>5</sub>-derived line with the pedigree 'KS94U216\*2/92R149'. KS94U216 is a HRWW experimental line developed from a bulk selection having the *Ae. tauschii*-derived gene *Lr21* conferring resistance to leaf rust. 92R149 is a spring wheat line developed at Nanjing Agricultural University having the gene *Pm21* conferring resistance to powdery mildew present on the translocation T6VS-6AL consisting of the short arm of the *H. villosa* chromosome 6V translocated to the long arm of wheat chromosome 6A. KS04WGRC48 was selected for resistance to leaf rust and powdery mildew in field evaluations at Manhattan, KS and at Lexington, KY.

Adult plants of KS04WGRC48 displayed no visible sign of leaf rust infection when exposed to moderate to heavy inoculum levels in the field at Manhattan and Hutchinson, KS, in 2003 and 2004, and small chlorotic flecks under heavy inoculum pressure at Castroville, TX, in 2004. Seedlings of KS04WGRC48 exhibited a low infection type (IT = 0; to ;1, small flecks or small pustules with chlorosis) when inoculated with races KDBL, PNMQ, MCDL, MFBL, and TNRJ of *P. tritricina*. High infection types (IT = 4, large pustules with little or no chlorosis) were observed on seedlings of the susceptible cultivar TAM 107 with all races of leaf rust tested. Presence of the 1.36-Kb fragment amplified by the primer pair KSUD14, which corresponds to a portion of the cloned *Lr21* gene, indicates that KS94U216 and KS04WGRC48 have *Lr21*. This gene provides effective resistance to all races of leaf rust in North America. No evidence of powdery mildew infection was noted on adult plants of KS04WGRC48 when exposed to heavy inoculum levels in the field at Hutchinson, KS, and Lexington, KY, in 2003 and 2004. Homogeneity of T6VS-6AL translocated chromosome in KS04WGRC48 was confirmed by amplification of the 1,265-bp DNA fragment expected with a SCAR marker linked to *Pm21* and lack of amplification of two wheat microsatellite markers located on 6AS. The *Pm21* gene provides effective resistance to all races of powdery mildew in North America.

### ***Notice of release of KS04WGRC49 hard winter wheat germ plasm with unique glutenin and gliadin proteins.***

G.L. Brown-Guedira (USDA-ARS); M. Guedira, and A.K. Fritz (Department of Agronomy); T.J. Martin (KSU Agricultural Research Center, Hays, KS); O.K. Chung, G.L. Lookhart, and B.W. Seabourn (USDA-ARS Grain Quality and Production Research Unit, Manhattan, KS); B.S. Gill; and T.S. Cox (Land Institute, Salina, KS).

KS04WGRC49 is a BC<sub>2</sub>F<sub>4</sub>-derived hard red winter wheat line from the cross 'Karl 92\*3/TA2473'. Karl 92 is a HRWW cultivar and TA2473 is an accession of *Ae. tauschii*. KS04WGRC49 was selected based on the presence of unique *Ae. tauschii*-derived HMW-gliadin protein subunits and novel HMW-glutenin protein subunits, designated 43 (allele *Glu-D1-1j*) and 44 (allele *Glu-D1-2i*). The effects of HMW-glutenin subunits 43 and 44 and the *Ae. tauschii*-derived gliadin proteins on the milling and baking quality of KS04WGRC49 were determined in experiments grown at Hays and Colby, KS, during the 1999 growing season and at Hays and Hutchinson, KS, during the 2001 growing season. Across locations, mixing time and mixing tolerance score of KS04WGRC49 (4.05 min and 4.47, respectively) were not significantly different ( $P = 0.05$ ) from that observed for Karl 92 (4.60 min and 4.24, respectively). KS04WGRC49 had significantly greater loaf volume (993 cc) than Karl 92 (946 cc) in these experiments. These data indicate that the novel glutenin and gliadin protein subunits in KS04WGRC49 can have the effects of increasing loaf volume while slightly decreasing mixing time.

**Seed requests of WGRC germ plasm lines.**

Small quantities (3 g) of KS04WGRC45, KS04WGRC46, KS04WGRC47, KS04WGRC48, and KS04WGRC49 seed, as well as previous releases (see WGRC web site for information) are available upon written request. We request that appropriate source be given when this germ plasm contributes to research or development of new cultivars. Seed stocks are maintained by the Wheat Genetics Resource Center, Throckmorton Hall, Kansas State University, Manhattan, KS 66506. Genetic material of this release will be deposited in the National Plant Germplasm System where it will be available for research purposes, including the development of new cultivars.

**Publications.**

- Conley EJ, Nduati V, Gonzalez-Hernandez JL, Mesfin A, Trudeau-Spanjers M, Chao S, Lazo GR, Hummel DD, Anderson OD, Qi LL, Gill BS, Echalié B, Linkiewicz AM, Dubcovsky J, Akhunov ED, Dvorak J, Peng JH, Lapitan NLV, Pathan MS, Nguyen HT, Ma X-F, Miftahudin, Gustafson JP, Greene RA, Sorrells ME, Hossain KG, Kalavacharla V, Kianian SF, Sidhu D, Dilbirligi M, Gill KS, Choi DW, Fenton RD, Close TJ, McGuire PE, Qualset CO, and Anderson JA. 2004. A 2600-locus chromosome bin map of wheat homeologous group 2 reveals interstitial gene-rich islands and colinearity with rice. *Genetics* 168:625-637.
- Dvorak J, Luo M-C, Dial KR, Thomas C, McGuire PE, Li W, Kuraparthi V, Gill BS, You FM, Gu Y-Q. 2005. Physical mapping of the *Aegilops tauschii* genome. *PAG XIII Abstracts*, P170, p. 40.
- Faris JD, Simons KJ, Fellers JP, Trick HN, and Gill BS. 2005. *Q*: a floral homeotic gene key to the domestication of wheat. *PAG XIII Abstracts*, W186, p. 44.
- Friebe B, Zhang P, Linc G, and Gill BS. 2005. Robertsonian translocations in wheat arise by centric misdivision of univalents at anaphase I and rejoining of broken centromeres during interkinesis of meiosis II. *Cytogenet Genome Res* 109:293-297.
- Gill BS. 2005. White paper on IGROW. *PAG XIII Abstracts*, W169, p. 40.
- Gill BS, Appels R, Botha-Oberholster A-M, Buell CR, Bennetzen JL, Chalhoub B, Chumley F, Dvorak J, Iwanaga M, Keller B, Li W, McCombie WR, Ogihara Y, Quétier F, and Sasaki T. 2004. A workshop report on wheat genome sequencing. The International Genome Research on Wheat Consortium. *Genetics* 168:1087-1096.
- Hossain KG, Kalavacharla V, Lazo GR, Hegstad J, Wentz MJ, Simons K, Gehlhar S, Rust JL, Syamala RR, Obeori K, Bhamidimarri S, Karunadharma P, Chao S, Anderson OD, Qi LL, Echalié B, Gill BS, Linkiewicz AM, Ratnasiri A, Dubcovsky J, Akhunov ED, Dvorak J, Miftahudin, Ross K, Gustafson JP, Sidhu D, Dilbirligi M, Gill KS, Peng JH, Lapitan NLV, Greene RA, Bermudez-Kandianis CE, Sorrells ME, Feril O, Pathan, MS, Nguyen HT, Gonzalez-Hernandez JL, Wennerlind EJ, Anderson JA, Fenton D, Close TJ, McGuire PE, Qualset CO, and Kianian SF. 2004. A chromosome bin map of 2148 EST loci of wheat homeologous group 7. *Genetics* 168:687-699.
- Kianian SF, Riera-Lizarazu O, Yadegari R, Dubcovsky J, Gill BS, Nelson JC, and Perrizo W. 2005. Development of diploid wheat (*Triticum monococcum*) deletion lines for reverse genetics. *PAG XIII Abstracts*, P757, p. 258.
- Kumar S, Friebe B, and Gill BS. 2005. Identification and mapping of gene rich bacs in wheat by FISH. *PAG XIII Abstracts*, P240, p. 133.
- Lazo GR, Chao S, Hummel DD, Edwards H, Crossman CC, Lui N, Matthews DE, Carollo VL, Hane DL, You FM, Butler GE, Miller RE, Close TJ, Peng JH, Lapitan NLV, Gustafson JP, Qi LL, Echalié BE, Gill BS, Dilbirligi M, Sandhu D, Gill KS, Greene RA, Sorrells ME, Akhunov ED, Dvorak J, Linkiewicz AM, Dubcovsky J, Hossain KG, Kalavacharla V, Kianian SF, Mahmoud AA, Miftahudin, Ma X-F, Wennerlind EJ, Anderson JA, Pathan MS, Nguyen HT, McGuire PE, Qualset CO, and Anderson OD. 2004. Development of an expressed sequence tag (EST) resource for wheat (*Triticum aestivum* L.): EST generation, unigene analysis, probe selection and bioinformatics for a 16,000-locus bin-delineated map. *Genetics* 168:585-593.
- Li W, Zhang P, Fellers JP, Friebe B, and Gill BS. 2004. Sequence composition, organization, and evolution of the core Triticeae genome. *Plant J* 40:500-511.
- Linkiewicz AM, Qi LL, Gill BS, Ratnasiri A, Echalié B, Chao S, Lazo GR, Hummel DD, Anderson OD, Akhunov ED, Dvorak J, Pathan MS, Nguyen HT, Peng JH, Lapitan NLV, Miftahudin, Gustafson JP, La Rota CM, Sorrells ME, Hossain KG, Kalavacharla V, Kianian SF, Sandhu D, Bondareva SN, Gill KS, Wennerlind EJ, Anderson JA, Fenton RD, Close TJ, McGuire PE, Qualset CO, and Dubcovsky J. 2004. A 2500-locus bin map of wheat homeologous group 5 provides insights on gene distribution and colinearity with rice. *Genetics* 168:665-676.
- Liu S, Pumphrey MO, Zhang X, Gill BS, Stack RW, Gill JS, Dolezel J, Chalhoub B, and Anderson JA. 2005. Toward positional cloning of *Qfhs.ndsu-3BS*, a major QTL for Fusarium head blight resistance in wheat. *PAG XIII Abstracts*, W307, p. 71.

- Massa AN, Morris CF, and Gill BS. 2004. Sequence diversity of puroindoline-a, puroindoline-b, and the grain softness protein genes in *Aegilops tauschii* Coss. *Crop Sci* 44:1808-1816.
- Miftahudin, Ross K, Ma X-F, Mahmoud AA, Layton J, Rodriguez M, Chikmawati T, Ramalingam J, Feril O, Pathan MS, Surlan Momirovic G, Kim S, Chema K, Fang P, Haule L, Struxness H, Birkes J, Yaghoubian C, Skinner R, McAllister J, Nguyen V, Qi LL, Gill BS, Linkiewicz AM, Dubcovsky J, Akhunov ED, Dvorak J, Dilbirligi M, Gill KS, Peng JH, Lapitan NLV, Bermudez-Kandianis CE, Sorrells ME, Hossain KG, Kalavacharla V, Kianian SF, Lazo GR, Chao S, Anderson OD, Gonzalez-Hernandez J, Wennerlind EJ, Anderson JA, Choi D-W, Fenton RD, Close TJ, McGuire PE, Qualset CO, Nguyen HT, and Gustafson JP. 2004. Analysis of EST loci on wheat chromosome group 4. *Genetics* 168:651-663.
- Mateos-Hernandez M, Singh RP, Hulbert S, Gill BS, and Brown-Guedira GL. 2005. Targeted mapping of wheat ESTs linked to the adult plant resistance gene *Lr46*. *PAG XIII Abstracts*, P339, p. 157.
- Munkvold JD, Greene RA, Bermudez-Kandianis CE, La Rota CM, Edwards H, Sorrells SF, Dake T, Benscher D, Kantety R, Linkiewicz AM, Dubcovsky J, Akhunov ED, Dvoak J, Miftahudin, Gustafson JP, Pathan MS, Nguyen HT, Matthews DE, Chao S, Lazo GR, Hummel DD, Anderson OD, Anderson JA, Gonzalez-Hernandez JL, Peng JH, Lapitan N, Qi LL, Echaliier B, Gill BS, Hossain KG, Kalavacharla V, Kianian SF, Sandhu D, Erayman M, Gill KS, McGuire PE, Qualset CO and Sorrells ME. 2004. Group 3 chromosome bin maps of wheat and their relationship to rice chromosome 1. *Genetics* 168:639-650.
- Peng JH, Zadeh H, Lazo GR, Gustafson JP, Chao S, Anderson OD, Qi LL, Echaliier B, Gill BS, Dilbirligi M, Sandhu D, Gill KS, Greene RA, Sorrells ME, Akhunov ED, Dvorak J, Linkiewicz AM, Dubcovsky J, Hossain KG, Kalavacharla V, Kianian SF, Mahmoud AA, Miftahudin, Wennerlind EJ, Anderson JA, Pathan MS, Nguyen HT, McGuire PE, Qualset CO, and Lapitan NLV. 2004. Chromosome bin map of expressed sequence tags in homeologous group 1 of hexaploid wheat and homeology with rice and *Arabidopsis*. *Genetics* 168:609-623.
- Qi LL, Echaliier B, Chao S, Lazo GR, Butler GE, Anderson OD, Akhunov ED, Dvorak J, Linkiewicz AM, Ratnasiri A, Dubcovsky J, Bermudez-Kandianis CE, Greene RA, Kantety R, La Rota CM, Munkvold JD, Sorrells SF, Sorrells ME, Dilbirligi M, Sidhu D, Erayman M, Randhawa HS, Sandhu D, Bondareva SN, Gill KS, Mahmoud AA, Ma X-F, Miftahudin, Gustafson JP, Wennerlind EJ, Nduati V, Gonzalez-Hernandez JL, Anderson JA, Peng JH, Lapitan NLV, Hossain KG, Kalavacharla V, Kianian SF, Pathan MS, Zhang DS, Nguyen HT, Choi D-W, Close TJ, McGuire PE, Qualset CO, and Gill BS. 2004. A chromosome bin map of 16,000 expressed sequence tag loci and distribution of genes among the three genomes of polyploid wheat. *Genetics* 168:701-712.
- Qi L, Friebe B, and Gill BS. 2005. Origin, structure, and behavior of a highly rearranged chromosome 1BS-4 in wheat. *PAG XIII Abstracts*, P238, p. 133.
- Randhawa HS, Dilbirligi M, Sidhu D, Erayman M, Sandhu D, Chao S, Lazo GR, Anderson OD, Miftahudin, Gustafson JP, Echaliier B, Qi LL, Gill BS, Akhunov ED, Dvorak J, Linkiewicz AM, Ratnasiri A, Dubcovsky J, Bermudez-Kandianis CE, Greene RA, Sorrells ME, Wennerlind EJ, Anderson JA, Peng JH, Lapitan NLV, Hossain KG, Kalavacharla V, Kianian SF, Pathan MS, Nguyen HT, Endo TR, Close TJ, McGuire PE, Qualset CO, and Gill KS. 2004. Deletion mapping of homeologous group 6-specific wheat ESTs. *Genetics* 168:677-686.
- Scofield SR, Huang L, Branch AS, and Gill BS. 2005. Functional pathogenomics in hexaploid wheat. *PAG XIII Abstracts*, W361, p. 60.
- Simons KJ, Fellers JP, Trick HN, Gill BS, and Faris JD. 2005. Isolation and characterization of the major domestication gene *Q* in wheat. *PAG XIII Abstracts*, P072, p. 97.
- Soria MA, Anderson JA, Brown-Guedira GL, Campbell, KG, Elias EM, Fritz AK, Gill BS, Gill KS, Haley S, Kianian SF, Kigdwell K, Laitan NLV, Ohm H, Sherman JD, Sorrells ME, Souza E, Talbert L, and Dubcovsky L. 2005. The MAS wheat project: impact of genomics on wheat breeding. *PAG XIII Abstracts*, P305, p. 149.
- Sorrells ME, La Rota M, Bermudez-Kandianis CE, Greene RA, Kantety R, Munkvold JD, Miftahudin, Mahmoud A, Ma X, Gustafson PJ, Qi LL, Echaliier B, Gill BS, Matthews DE, Lazo GR, Chao S, Anderson OD, Edwards H, Linkiewicz AM, Dubcovsky J, Akhunov ED, Dvorak J, Zhang D, Nguyen HT, Peng J, Lapitan NLV, Gonzalez-Hernandez JL, Anderson JA, Hossain K, Kalavacharla V, Kianian SF, Choi D-W, Close TJ, Dilbirligi M, Gill KS, Steber C, Walker-Simmons MK, McGuire PE, and Qualset CO. 2003. Comparative DNA sequence analysis of wheat and rice genomes. *Genome Res* 13:1818-1827.
- Yu, J-K, Dake TM, Singh S, Benscher D, Li W, Gill BS, and Sorrells ME. 2004. Development and mapping of EST-derived simple sequence repeat markers for hexaploid wheat. *Genome* 47:805-818.
- Zhang P, Li W, Friebe B, and Gill BS. 2004. Simultaneous painting of three genomes in hexaploid wheat by BAC-FISH. *Genome* 47:979-987.

**GRAIN MARKETING AND PRODUCTION RESEARCH CENTER****U.S. Grain Marketing Research Laboratory, USDA, Agricultural Research Service,  
Manhattan, KS 66502, USA.**

O.K. Chung, F.E. Dowell, S.H. Park, G.L. Lookhart, M. Tilley, D.L. Brabec, M.S. Ram, L.M. Seitz, S.R. Bean, B.W. Seabourn, T.C. Pearson, D.B. Bechtel, M.E. Casada, J.D. Hubbard, J.D. Downing, E.B. Maghirang, J.D. Wilson, P.R. Armstrong, M.S. Caley, F. Xie, F.H. Arthur, R.K. Lyne, and S.Z. Xiao.

***How wheat breeding brings benefits for users and consumers.***

O.K. Chung.

In spite of a lengthy and costly process of 12–13 years, wheat breeders must continue to develop and release new cultivars, as older cultivars tend to lose disease and pest resistance over 3–5 years. Three broad stages of breeding are the 1st stage (years 1 and 2) of mating, the 2nd stage (years 3–7) of inbreeding and selection, and the last stage (years 8–12) of evaluation of breeding lines. Both genotype and wheat-growing environment (soil and climate) greatly influence the growth of plant, seed production, and the end-use quality. Breeding selects lines based on genotypic superiority of agronomic and end-use quality as well as the environmental stability on its growth and end-use quality. Additionally, wheat-exporting countries have to provide wheat with quality traits vital to the importing customers' own unique products. Active breeding programs of public and private sectors, or their corporative entities, share the common objectives: to improve agronomic, disease, and pest resistance so that wheat producers can enjoy high yield, wheat users (milling/baking industry) can have milling and end-use quality traits, while ensuring consumer satisfaction in the final products. Thus, 'breeding for quality, tailored for specific products' is the concerted efforts of all sectors, including cereal chemist/food technologists. The type of quality testing or definition of quality differs somewhat among different countries and it will be discussed in this presentation.

***Roles of the four ARS regional wheat quality laboratories in U.S. wheat quality improvement.***

O.K. Chung, C.S. Gaines, C.F. Morris, and G.A. Hareland.

Wheat quality improvement begins with breeding. Important traits targeted in wheat breeding include both agronomic and end-use quality. The current U.S. Standards categorize wheat into eight basic classes based on color, hardness, and growing season. Each wheat class is traditionally grown in a specific region in the U.S. The USDA–ARS Regional Wheat Quality Laboratories (RWQLs) were established by an Act of Congress: the Soft Wheat Quality Lab in 1936, the Hard Winter Wheat Quality Lab in 1937, the Western Wheat Quality Lab in 1946, and the Hard Red Spring and Durum Wheat Quality Lab in 1963. All four RWQLs have common missions: work with breeders to improve U.S. wheat by testing end-use quality of experimental breeding lines, develop reliable small-scale tests for evaluating early generation breeding lines, perform research on the contribution of flour biochemical components to observed differences in end-use quality, conduct research on molecular-genetic bases of quality, and develop rapid and objective prediction models for end-use quality. All four RWQLs focus primarily on the public (university and USDA–ARS) breeding lines and some private breeding lines. Over 95 % of U.S. wheat released cultivars have been evaluated at one of the RWQLs. Therefore, the RWQLs have made paramount contributions to U.S. wheat quality improvements for all wheat classes. This presentation will describe the activity of each RWQL.

***Quality parameters of four wheat fractions singulated and sorted based on kernel hardness.***

O.K. Chung, E.B. Maghirang, S.H. Park, M.S. Caley, F.E. Dowell, and B.W. Seabourn.

Two pure HWW lines, NE98471 and NI98439, harvested in 2002 and entered into the HWW Quality Council Testing in 2003, were graded as mixed wheat by the FGIS classification, using a SKCS 4100. We investigated if there were differences in wheat and flour quality parameters among the fractions with different single kernel hardness index (SK-

HI) of the same HWW lines. Each bulk of two lines was singulated and sorted into four fractions by a Perten SK-NIR Sorter. The average SK-HI was 47 for NE98471 (L1) and the sorted fractions (f1, f2, f3, and f4) showed the average SK-HI of 41, 46, 50, and 53, respectively. The average SK-HI was 46 for NI98439 (L2) and the HI values were 34, 40, 46, and 53, respectively, for f1 to f4. The L2-f1 and f2 were classified as soft wheat. Wheat physical parameters, including micro-test weight (TW), SK-weight (WT), SK-size (SZ), and micro-milling yield decreased in the sorted fraction with increasing SK-HI. However, wheat chemical parameters, including protein (PC) and ash contents (AC), increased in the fractions with increasing HI. Accordingly, the flour PC and AC increased. Both mixograph and micro-bake (10-g flour) water absorptions and mix times, as well as bread volumes, increased with increasing SK-HI in sorted fractions. The trends were more pronounced with L2 fractions than with L1 fractions.

### ***A comparison of a Farinograph (10-g flour) with variable mixing speed to a mixograph (10-g flour) in flour-quality testing.***

O.K. Chung and S.H. Park.

A mixograph (10-g flour) (MIXO) has greatly contributed to the HWW breeding programs in screening early-generation lines based on mixing quality. Although a farinograph provides similar data and is used by industry worldwide, it has not been used for breeding programs, due to its large flour requirement (50 g) and longer testing time. The Farinograph® E (FARINO) can be used with the standard test (63/min) as well as at other variable speeds. In addition, a mini-mixing bowl (10-g flour) is currently available. We investigated mixing quality of 4 HWW (6.9, 12.6, 12.7, and 14.8 % flour protein) with a FARINO at the 63, 75, 88, and 100/min mix speed and a MIXO at the 88/min speed. Water absorption (WA) increased (6.2 % on average) whereas mix-time (MT), stability, and the time to break decreased (36, 60, and 32 %, respectively) with an increased mix speed from 63 to 100/min (59 %). The WA and MT of the 4 flours averaged 64.9 % and 6.84 min for the FARINO (at 88/min), whereas 62.3 % and 3.30 min for the MIXO, respectively. The FARINO-WA was significantly correlated with bake-WA and bread volume at all 4 speeds but better at the higher speed (88 and 100/min), which also was significantly correlated to MIXO-WA. Although the average FARINO-MT was still about 180 % of MIXO-MT even at the 100/min with much thinner curve, the reduction of MT by 36 % shows a potential use for breeding programs.

### ***Measuring wheat starch size distribution using image analysis and laser-diffraction technology.***

J.D. Wilson and D.B. Bechtel.

Particle size and shape has long been recognized as an important variable in a range of processes including predicting rheology and flow behavior. Wheat, barley, rye, and triticale have starch populations with multimodal distributions; large A-type granules lenticular in shape and smaller B- and C-type granules spherical in shape. A wide range in particle size creates difficulties in accurately measuring starch populations. Starch, isolated from flour of four classes of wheat, was analyzed by digital image analysis (IA) and laser diffraction sizing (LDS) to measure starch size distributions. IA data was converted to volume percent to be compared to LDS data. IA errors were detected, corrected, and compared with size distributions obtained from LDS. LDS resulted in a ~40 % underestimation of the A-type granule diameter and a ~50 % underestimation of the B-type granule diameter in comparison to IA. Laser diffraction data correlated to IA data, with R<sup>2</sup> values ranging from 0.02 (not significant) to 0.55\*\*\*. A correction factor was used to adjust LDS and IA data for better correlations. After the adjustment, correlations improved (R<sup>2</sup> = 0.79\*\*\* to 0.93\*\*\*) depending on the class of wheat starch evaluated. This work represents a step towards combining IA and LDS technologies to study nonspherical particles.

### ***Laser-diffraction sizing used to study wheat flour and starch particle sizes.***

D.B. Bechtel and J.D. Wilson.

Predicting wheat quality is an important goal of the grain industry. Laser-diffraction sizing (LDS) was used to measure particle size distributions of wheat flour and isolated starch to determine if the method could be used as a component for predicting end-use quality. Five HRWW and five SRWW were milled into flour from which starch was isolated. Flour

particle size distributions were measured using a dry module as well as flour suspended in isopropanol (AACC Method 55–40). Analysis using isopropanol as a suspension fluid caused smaller particles ( $< 8$  Fm in diameter) to be released from flour. Use of isopropanol caused a shift to larger particle sizes between 8 and 400 Fm in comparison to dry analysis. Isopropanol also caused clumping with spurious particles found between 250–400 Fm. LDS of isolated starch showed a separation of A- and B-type granules between 9.8 and 10.8 Fm for the soft wheats and between 8.2 and 9.8 Fm for hard wheats. Hard wheats had a larger volume of starch in the A-type fraction while the soft wheats had more starch in B- and C-type fractions. A demarcation between the B- and C-type starch was only observed for the soft wheats and that was when data was presented as percent surface area. LDS may prove to be a valuable tool in helping predict wheat end-use quality since flour and starch differences were observed between wheat classes as well as among wheats within a class.

### ***Size distribution and properties of wheat starch granules in relation to crumb grain score of pup-loaf bread.***

S.H. Park, O.K. Chung, and P.A. Seib.

Twelve hard winter wheat flours with protein contents of 11.8–13.6 % (14 % mb) were selected to investigate starch properties associated with the crumb grain score of experimentally baked pup-loaf bread. The 12 flours were classified in four groups depending on the crumb grain scores which ranged from 1 (questionable-unsatisfactory) to 4 (satisfactory). Flours in groups 1, 2, 3, and 4 produced breads with pup-loaf volumes ranging from 910 to 1,035, 1,000 to 1,005, 950 to 1,025, and 955 to 1,010 cm<sup>3</sup>, respectively. Starches were isolated by a dough hand-washing method and purified by washing to give 75–79 % combined yield (dry flour basis) of prime (62–71 %) and tailing (7–16 %) starches. The prime starch was fractionated further into large A-granules and small B-granules by repeated sedimentation in aqueous slurry. All starches were assayed for weight percentage (wt%) of B-granules, swelling power (92.5°C), amylose content, and granular size distribution by quantitative digital image analysis. A positive linear correlation was found between the crumb grain scores and the A-granule sizes ( $r = 0.65$ ,  $P < 0.05$ ), and a polynomial relationship ( $r = 0.67$ ,  $P < 0.05$ ) occurred between the score and the wt% of B-granule starch. The best crumb grain score was obtained when a flour had a wt% of B-granules from 19.8 to 22.5 %, shown by varietal effects.

### ***Effects of varying weight ratios of large and small wheat starch granules on experimental straight-dough bread.***

S.H. Park, O.K. Chung, and P.A. Seib.

One commercial bread wheat flour with medium strength (11.3 % protein content on 14 % mb) was fractionated into three fractions (starch, gluten, and water-solubles) by hand-washing. The starch fraction was further separated into large and small granules (LG and SG) by repeated sedimentation. Sizes of large (10–40  $\mu$ m in diameter) and small (1–15  $\mu$ m in diameter) starch fractions were examined. Flour fractions were reconstituted to their original levels in the flour, using composites of varying weight percentages of starch granules: SG being 0 % (100 % LG), 30 %, 60 %, and 100 % (0 % LG). A modified straight-dough method was used in an experimental baking test. Crumb grain and texture were significantly affected: the bread made from the reconstituted flour with 30 % SG and 70 % LG starch had the highest crumb grain score (4.0, subjective method), the peak fineness value (1029) and the second highest elongation ratio (1.55). Inferior crumb grain scores, low fineness and elongation ratios were observed in breads made from flours with starch fractions at 100 % SG or 100 % LG. Because the proportion of SG increased in the reconstituted flour, it yielded bread with softer texture that was better maintained than the bread made from the reconstituted reference flour during storage.

***Lipid extraction from wheat flour using supercritical fluid extraction.***

J.D. Hubbard, J.D. Downing, M.S. Ram, and O.K. Chung.

Environmental concerns, the disposal cost of hazardous waste, and the time required for extraction in current methods encouraged us to develop an alternate method for analysis of wheat flour lipids. Supercritical fluid extraction (SFE) with CO<sub>2</sub> has provided that medium and the method is fully automatic. Crude fats or nonstarch free lipids (FL) were extracted from 4–5 g of wheat flour by an SFE system. To develop optimum conditions for SFE, various extraction pressures, temperatures, and modifier volumes were tried to provide a method that would produce an amount of lipids comparable to those extracted by the AACC Approved Soxhlet Method and the AOCS Official Butt Method using petroleum ether as solvent. Using several wheat flour samples, the best conditions were 12.0 vol % ethanol (10.8 mol %) at 7,500 psi and 80°C to extend the amount of FL similar to those by the AACC and AOCS methods. Using solid-phase extraction, lipids were separated into nonpolar lipid (NL), glycolipid (GL), and phospholipid (PL) fractions. The mean value of 5 flours was 1.15 % (flour wt., db) by the SFE method, 1.07% by the Butt method, and 1.01 % by the Soxhlet method. The SFE-extracted lipids contained less NL and more GL than either the Butt or Soxhlet methods. All three methods extracted lipids with quality similar components. The overall benefit for SFE over the Soxhlet or Butt methods was to increase the number of samples analyzed in a given time, reduce the cost of analyze, and reduce exposure to toxic chemicals.

***Wheat flour lipids extracted by a dual-pump CO<sub>2</sub>-ethanol supercritical fluid extraction system.***

M.S. Ram and O.K. Chung.

Supercritical fluid CO<sub>2</sub> (SF-CO<sub>2</sub>) is a useful system for extracting nonpolar lipids (NL) from wheat flour. However, a polar modifier, such as ethanol, is necessary to extract the polar lipids (PoL) and the amount of lipids extracted by a supercritical fluid extraction (SFE) system varies with the % modifier used (Fig. 1). In our research the extracted lipids were fractionated on silica solid-phase extraction cartridges to obtain the NL and PoL composition. Previously, we have reported that SF-CO<sub>2</sub> at 7,500 psi and 80°C with 12 % (v/v) ethanol as a modifier extracted all the free lipids (FL) from wheat flour (Hubbard JD et al. Cereal Chem, In press). The objective of this study was to test the feasibility of sequentially extracting FL from wheat flour so that we do not have to fractionate the extracted FL in to the NL and PoL fractions. We have used four HRWW flours to develop the sequential extraction (SEx) method for flour FL using SFE. First, the NL fraction of flour FL was extracted by using SF-CO<sub>2</sub> only (1st SEx), and then the PoL fraction was extracted with the addition of modifier ethanol to SF-CO<sub>2</sub> (2nd SEx). Lipids were extracted by SEx and the one-step SFE method from four flours. The amounts of lipids extracted by 1st and 2nd SEx were in agreement with the amounts of NL and PoL fractionated from the FL by the one-step extraction. The success of the sequential extraction is evidenced by the TLC chromatograms in which the individual components of NL and PoL could be qualitatively determined. The 1st SEx contained NL only, and the 2nd SEx contained only PoL that did not migrate. Extracted by the one-step SFE method, they contained both NL and PoL. These results indicate that we succeeded in our goal of fractionating wheat flour lipids using SEx without the need for a separate fractionation step after the SFE extraction.

***Sequential extraction of nonpolar and polar classes of wheat flour lipids using supercritical-carbon dioxide with ethanol modifier.***

M.S. Ram and O.K. Chung.

Wheat flour free lipids (FL), a minor constituent, play significant roles in breadmaking and contribute to bread quality prediction as the secondary quality determinant (QD) with flour protein as the primary QD. The ratios of nonpolar (NL) to polar lipids (PoL) in FL of given flours are inversely related to the size of bread baked from the corresponding flours. To obtain this ratio, we need to perform two steps, extraction and fractionation. Our objective was to develop a one-step procedure that will sequentially extract NL, followed by PoL, using supercritical-fluid extraction (SFE) by optimizing the pressure (P), temperature (T) and modifier concentration. Extraction parameters were varied for P (4,500–7,500 psi), T (60–80°C), and modifier (0 or 11% mole fraction, ethanol). Four flour samples were first extracted with 0% modifier at varying P and T, followed by one at P = 7,500 psi, T = 80°C and 11 % ethanol (SFE1). The SFE1 condition alone can extract lipids of 0.63 % NL and 0.37 % PoL, fractionated by the solid-phase-extraction cartridges. Those quantities of

NL and PoL were matched by that obtained in sequential SFE conditions (6,500 psi and 60°C followed by SFE1). The new one-step SFE procedure can perform the dual steps of extraction and fractionation and determine the NL/PoL ratios of many samples/day. Thus, it might be able to screen early generation wheat breeding lines, based on FL composition.

### ***A microbaking procedure: Its relation to pup straight-dough and pound sponge and dough baking methods.***

M.S. Caley, S.H. Park, and O.K. Chung.

A microbaking (MB) procedure of 10-g flour is an invaluable analytical tool for special research projects, including some unique germplasm, at the Hard Winter Wheat Quality Laboratory. We use the pup straight dough (PSTD) method of 100-g flour, as a routine method for testing HWW breeding lines. In addition, we have the pound sponge and dough (PS&D) method, most commonly used at the baking industry, of 300-g flour to test wheat breeding lines at the advanced stages, just prior to its release, such as lines entered into the Wheat Quality Council testing. The objective of this study was to investigate the relationships of those three baking methods. We used 51 flours (18 HWW and 33 hard spring wheat) from lines harvested in 2003 and entered into the 2004 Wheat Quality Council testing. Many bake parameters of the MB procedure were highly significantly correlated to that of other two procedures including: the water absorption (WA) of MB to the PSTD-WA ( $r = 0.99$ ) and PS&D-WA ( $r = 0.97$ ); the mix time (MT) of MB to the PSTD-MT ( $r = 0.97$ ) and PS&D-MT ( $r = 0.70$ ); the loaf volume (LV) of the MB to the PSTD-LV ( $r = 0.91$ ) and PS&D-LV ( $r = 0.75$ ); and the crumb grain score (CGS) of MB to the PSTD-CGS ( $r = 0.58$ ,  $P < 0.0001$ ) and the PS&D-CGS ( $r = 0.43$ ,  $P < 0.005$ ). The MB parameters were related more closely to the pup than to the pound procedures, in part, due to the same straight-dough formula between the MB and the PSTD procedures.

### ***Rapid determination of dough-mixing requirement for early generation breeding lines by FT-HATR mid-Infrared (IR) spectroscopy.***

B.W. Seabourn, F. Xie, and O.K. Chung.

The optimum mix time (MT) in a wheat flour-water (dough) system is an important rheological property to wheat breeders in screening germplasm and early generation breeding lines for end-use functionality, i.e., bread quality. The traditional method of choice in the U.S. for screening HWW breeding lines, based on optimum MT, is the mixograph (MIXO), which is largely time-consuming in its method and somewhat subjective in its interpretation, especially with regard to mixing tolerance. In previous work, the authors showed the potential of using FT-HATR mid-IR spectroscopy as an objective measure to estimate wheat flour MT early in the dough mixing cycle. Seventeen HRW wheat flours with varying protein contents (~11–14 %) and MT's (1.63–7.38 min) were used in this preliminary study. Doughs (three replicates each) were scanned in the amide III region of the mid-IR (4,000–700/cm) by FT-HATR immediately after being mixed with a MIXO for 1 min. The ratio of the second derivative band areas at 1,335/cm (helix) and 1,242/cm (sheet) was highly correlated to optimum MT as determined by the MIXO ( $R^2 = 0.81$ ). Results obtained from this study indicated that this method has tremendous potential to rapidly determine optimum MT very early in the mixing process, solely based upon the chemistry of the system, with specific application to screening samples in breeding programs.

### ***Testing four solvents for solvent retention capacity (SRC) in hard winter wheat flour and their use in a regression equation to predict bread loaf volume.***

Z.S. Xiao, S.H. Park, O.K. Chung, M.S. Caley, and P.A. Seib.

We investigated the suitability of SRC in assessing HWW product quality. We measured the SRC values of 116 HWW samples with 5 % lactic acid (LA), 50 % sucrose (SU), 5 % sodium carbonate (SC), and water. We also tested quality parameters using methods such as SKCS, NIR spectroscopy, mixograph (Mixo), SDS sedimentation (SD), and breadmaking. The SRC values were highly dependent on the wheat/flour protein content, SK weight, diameter, and hardness, and 1,000-kernel weight. Bread loaf volume (LV) was most significantly correlated with the SRC by LA, followed by SU, and least by SC and water. Mixo-mix tolerance was correlated significantly with LA-SRC. The time x-

value of Mixo was notably correlated with LA-SRC and bread LV ( $R^2$  squared). SDS-SD volume and LA-SRC were both good indicators of LV. A prediction model for LV ( $R^2$ ) was developed by stepwise multiple regression analysis of the wheat and flour quality parameters plus the LA-SRC values of the 116 samples in the calibration set. An  $R^2$  value of 0.78 was observed for the validation set of 41 randomly chosen samples. The inclusion of 5 % LA-SRC value in the prediction model significantly increased  $R^2$  of both calibration and validation sets from 0.64 and 0.74, respectively, to 0.78. Among the four solvents, 5 % LA proved best for assessing HWW product quality, LV.

### ***Effect of dough weight and production method on wheat flour tortilla quality.***

J.N. Alviola, S. Arora, R.K. Lyne, G.L. Lookhart, R.D. Waniska, and O.K. Chung.

Several labs desire to evaluate wheat flours for tortilla quality without using pilot-scale, commercial equipment, and/or trained personnel. We evaluated how procedures using lab-scale equipment with two dough sizes compare to commercial tortillas prepared using pilot-scale commercial equipment. Twelve wheat flours varying in tortilla-making qualities were prepared into tortillas. Three dough-ball, pressing procedures were compared: the tortilla bake test prepared using pilot-scale, commercial equipment (Lawrence equipment) and a lab-scale method using a heated hand-press (Dough Pro 2000) with either Teflon-sheet-covered platens (80°C, 6 sec; DP-Teflon) or with use of an oil spray (74°C, 6 sec; DP-oil). Hand-pressed tortillas were baked on a griddle. A smaller dough size, 25 g instead of 42 g, was also hand-pressed using the Dough-Pro methods. The critical tortilla properties of diameter, opacity and shelf-stability were evaluated. Even though the three procedures (42-g dough) had similar average tortilla diameters and rollability scores at 12 days, the cultivars were not differentiated in the same order by rollability scores using the three procedures. Tortilla opacities were higher when prepared using the DP-oil method (86.6 %) than the DP-Teflon method (83.3 %) or Lawrence method (83.8 %). Specific volumes were higher for Dough-Pro pressed tortillas (25 and 42 g dough) compared to Lawrence-pressed tortillas. Thinner, smaller diameter tortillas with higher rollability scores after 12-days storage were formed using smaller dough size (25 g). These tortillas had opacities similar to DP-oil-pressed tortillas (42-g dough). The smaller dough size (25 g) yielded tortillas with different tortilla properties when compared to lab procedures using 42-g dough. The DP-oil or DP-Teflon method using 42-g dough procedures can be utilized when amount of flour is limited, such as early-generation variety testing.

### ***Correlation of wheat protein composition and dough rheological properties to tortilla quality.***

H. Singh, R.K. Lyne, O.K. Chung, S.H. Park, and G.L. Lookhart.

Protein composition and dough rheology of 15 wheat lines were studied. Total protein content and the ratio of polymeric to monomeric proteins (pk1/pk2) in SE-HPLC chromatograms of SDS extracts were correlated with tortilla-rollability scores (TRS) ( $R^2 = 0.51$  and  $0.59$ , respectively). However, the amounts of insoluble and soluble proteins were not significantly correlated to TRS. Stress relaxation (SR) and dough extensibility (DE) tests were conducted using a texture analyzer. Consistent results were obtained at 10 % strain level for doughs mixed for 5 min. Maximum resistance ( $R_{max}$ ) to extension during DE test and  $k_2$  (a measure of elasticity) during SR test correlated well with 12th day TRS ( $R^2 = 0.55$  and  $0.48$ , respectively). Poor-quality dough was less elastic with lower  $k_2$  values. The extensibility of dough was correlated significantly with the pk1/pk2 ratio ( $R$ -squared of  $0.64$ ), indicating a good relationship between molecular composition of proteins and rheological property of the dough. Multivariate analysis of protein and dough characteristics showed that a combination of Ext, relaxation time and the pk1/pk2 ratio had a highly significant correlation ( $R^2 = 0.94$ ) with TRS.

### ***Effects of flour properties on tortilla quality.***

R.D. Waniska, M. Cepeda, B.S. King, J.L. Adams, L.W. Rooney, P.I. Torres, G.L. Lookhart, S.R. Bean, J.D. Wilson, D.B. Bechtel.

Sixty-one commercial tortilla flours were tested for tortilla properties using a standardized tortilla bake test. Flour, dough, and tortilla properties were evaluated. All flours tested yielded tortillas with acceptable appearance and opacity, attributes important for the tortilla market. Twenty-eight of the tortilla flours yielded tortillas with a larger diameter,

longer shelf stability, and higher moisture content, attributes that are desirable for many retail and wholesale markets. Data for the flours tested confirmed the results of previous tortilla research, i.e., more protein or damaged starch in the flour corresponded to smaller diameter tortillas with improved storage stability and intermediate protein content yielded better quality tortillas. Data from the 28 flours yielding good quality tortillas provided more support for the impact of damaged starch and less support for the impact of proteins on tortilla quality: 1) tortilla diameter correlated with A starch granules and negatively with B starch granules and damaged starch measured by enzyme-susceptible starch (ESS); 2) tortilla stability correlated with mixing time and damaged starch measured by ESS and negatively with resistance to mixing; and 3) tortilla moisture content correlated with amounts of insoluble polymeric protein, soluble polymeric protein, and gliadin. The flour qualities needed to yield good quality tortillas are not well defined; however, components should include protein content (10.0–12.0 %), intermediate protein quality, and lower levels of starch damage during milling.

### ***PCR amplification of wheat sequences from DNA extracted during milling and baking.***

M. Tilley.

DNA-based analyses are highly sensitive and specific. Because processing steps can have profound effects on the proteins and DNA present in foods, this project examined the effects of breadmaking on wheat DNA size and PCR-based detection of sequences. DNA was extracted from wheat kernels, milling fractions, and flour, and from samples taken at various steps during and after the baking process. Kernels contained primarily high molecular weight DNA (>12,000 bp), whereas flour DNA exhibited a broad range of molecular weights from >12,000 bp to <300 bp. A marked reduction in DNA yield and size occurred after the first five minutes of baking. PCR successfully amplified products of both high and low copy number genes, even from DNA extracted from bread loaves five days after baking. However, successful amplification required that the maximum product size be no more than the average molecular weight of the DNA recovered from the source. The data also demonstrate that PCR can be used to detect the presence of yeast (*Saccharomyces cerevisiae*) a minor ingredient.

### ***Kernel, mixing, and baking characteristics of transgenic wheats with varying HMW-GS contents.***

A.E. Blechl, O.K. Chung, P.P. Bregitzer, J. Dubcovsky, and P. Sebesta.

In order to understand the structural basis of the functional role played by HMW-glutenin subunits in wheat end-use properties, we used genetic transformation to make wheats containing transgenes expressing natural HMW-glutenin subunits Ax2\*, Dx5, and/or Dy10 or variants of subunit Dx5. All the transgenics were derived from the cultivar Bobwhite. In 2002, we grew these lines and their non-transgenic parent in replicated plots at three locations. Samples of sixteen of these wheats from each location were submitted to extensive quality testing. We observed little variation in kernel and milling characteristics among the transgenic wheats and compared to the nontransformed parent. In contrast, flours from these wheats exhibited a wide range of dough and bread-making performance. Mixing and baking variability due to changes in HMW-glutenin content far exceeded variability attributable to the transformation process, environment, or flour protein levels. These results show that using biotechnology to change HMW-glutenin subunits content yields a wide range of flour end-use properties.

### ***Modifying tyrosine crosslink formation in wheat dough by controlling innate enzymatic activity.***

M. Tilley and K.A. Tilley.

Dityrosine (DY) is one of several crosslinks found in biological protein polymer systems, including plants and food matrices. Protein crosslinking via DY formation is initiated by free-radical oxidation and/or enzymatic methods. Peroxidase is commonly used to catalyze DY and related bonds. DY was found recently to form during mixing and baking of wheat flour. The water-soluble extract (WSE) from wheat flour, contain several biologically active enzyme systems and has the ability to catalyze DY formation. The albumin fraction (water soluble extract, WSE) was fractionated via preparative isoelectric focusing and resulting fractions were collected and tested for ability to form DY from free tyrosine. Proteins in the most reactive fractions were purified by cation exchange chromatography and subjected to N-

terminal amino sequencing. The fraction that catalyzed the greatest amount of DY contained a predominant 38-kDa protein that was determined to have the N-terminal sequence: AEPPVARGLSFDFYRRTPRAES. cDNA libraries from developing wheat kernels and *Ae. tauschii* were screened and isolated cDNAs were sequenced. The resulting cDNAs of 1,197 (*T. aestivum* subsp. *aestivum*) and 1191 (*Ae. tauschii*) nucleotides both have an open reading frame of 1,077 nucleotides and encode a protein of 358 amino acids with a 26 amino-acid signal sequence. The sequence has 90.4 % identity at the nucleotide level and 89 % identity at the amino-acid level with barley endosperm-specific cationic peroxidase BP1. Comparison to other peroxidase sequences from non-endosperm tissues of wheat display 40–45 % similarity, however amino-acid residues of the active site are highly conserved. The identification of endogenous components that catalyze DY may provide a means of predicting and controlling breadmaking quality.

### ***Comparison of the endoproteinases of various grains.***

B.L. Jones and G.L. Lookhart.

Two-dimensional IEF x PAGE gels were used to compare the endoproteolytic (gelatinase) activities of germinated barley to those of bread and durum wheats, rye, triticale, oats, rice, buckwheat, and sorghums. Barley was used as the standard of comparison because its endoproteinase complement has been studied in the greatest detail. The characteristics of the grain proteases were appraised from their migration patterns and by how they were affected by pH. All of the germinated grains contained multiple enzyme activities and their separation patterns and pH characteristics were at least similar to those of barley. The proteinases of the bread and durum wheats, ryes, oats, and sorghums were most similar to those of barley, whereas the other grains provided more varied patterns. The rice and buckwheat proteinases developed much more slowly than those of the other grains. The activity patterns of the triticales resembled those of their parents, wheat and rye, but the triticale contained many more activities and higher overall proteolytic activities than any of the other species. These results should be applied to scientific and/or commercial procedures with caution, because grains contain potent endogenous proteinase inhibitors that could inactivate these enzymes in various tissues and/or germination stages.

### ***Changes in tyrosine, dityrosine, and phosphotyrosine content in wheat cultivars exposed to heat stress.***

E. Reamer, M. Tilley, P. Srivarin, and K.A. Tilley.

Five unique wheat cultivars were subjected to control (25/20°C, day/night) and high temperature conditions (32/25°C) during kernel development in order to examine the changes in levels of tyrosine, dityrosine, and phosphotyrosine glutenin proteins. Heat stress conditions during wheat grain-filling period have implicated in contributing to the detrimental effects heat stress has on the bread-making properties of particular flours. Triplicate samples were taken for each cultivar under control and experimental conditions at 30 days post anthesis, which allowed experimental samples to be exposed to the heat stress conditions for approximately 20 to 30 days prior to sample collection. Following a sample preparation procedure in which bran and germ components were removed from the wheat kernels, glutenin proteins were extracted. The glutenin extraction was then followed by acid hydrolysis procedures and derivitization of the reconstituted hydrolysate prior to amino acid analysis with RP-HPLC. Results from the amino-acid analyses were compared with eight-point standard curves prepared from external standards in order to determine the concentrations (ng/μL) of each compound in control and experimental samples. These results showed that experimental samples exposed to the high temperature conditions consistently displayed increases in the concentrations of each of the compounds studied, with the most dramatic increases occurring in phosphotyrosine content.

### ***Wheat quality and wheat cultivar identification.***

G.L. Lookhart, S.R. Bean, and C.T. Culbertson.

The ability to identify wheat at all stages of its growth and use is very important to many people. Quality is in the eye of the beholder! A farmer might define quality as the amount of grain produced in the field, a miller might define it as the amount of flour that can be produced from a given amount of wheat on a given mill, a baker might define it as the type of

consistent product they can make from a given flour, and a breeder might define it as the overall the grain yield, which is a function of the plants' resistance to disease and drought, and the type of products that can be made from a given line. In each of these reasonable definitions, genetic, environmental, and 'genetic x environmental' components are present. Since we cannot control the environment, it is important to control or identify the genetics. Wheat gliadins are a genotypic expression of the plant and therefore characterizing the gliadins can be used to fingerprint wheat genotypes. Cultivar identification can be accomplished by any of three broad ways; agronomic, physical, or biochemical.

### ***The effect of wheat genetic background and growing conditions on the glutenin macro-polymer.***

C. Don, G.L. Lookhart, H. Naeem, F. MacRitchie, and R.J. Hamer.

Wheat quality is governed by both genetic and environmental factors. The quality of any given variety varies due to growing conditions and some cultivars are more susceptible than others. The effects of heat stress on the gluten macropolymers of mature NILs of Lance C and Lance A varying only in HMWGS 5+10 and 2+12, respectively, and Warigal A and Warigal C also varying only in 5+10 and 2+12, respectively, were studied. Wheat plants were grown under controlled conditions, using various temperature regimes to simulate six different stress levels. Treatment 1, control, involved growing the plants for the entire cycle at 20°C day/16°C night. Treatment 2 consisted of 30°C day/18°C night temperatures starting at 16 days after anthesis and continuing for 3 days and then returning to the control conditions. Treatment 3 was 35°C day and 20°C night starting at 16 days after anthesis and continuing for 3 days and then returning to the control conditions. Treatment 4 was 35°C day 20°C night starting at 16 days after anthesis and continuing until maturity. Treatment 5 was 40°C day and 25°C night starting at 16 days after anthesis and continuing until maturity. Heat stress increased going from treatment 1 to 5. SDS-insoluble/SDS-soluble ratios were least in Treatment 5, indicating that heat stress mainly affects GMP quantity. Clearly, the quantity of insoluble glutenin fractions like GMP and UPP, played an important role in wheat flour dough mixing properties. A Coulter Scanning Laser Microscope was used to detect GMP particles. The particle size measurements, for all varieties, indicated that more large particles are shown in heat stressed samples than in samples grown under mild conditions and severely heat stressed samples have very large glutenin particles, > 100 µm. The presence of much larger amounts of SDS soluble proteins over SDS insoluble proteins in severely stressed samples was observed.

### ***All-grain home brewing.***

D.B. Bechtel.

Beer occurs in two basic styles; lagers and ales. The only difference being the type of yeast used to brew the beer. All-grain brewing at home uses whole grain malts (as well as unmalted grain adjuncts) of various types to control flavor and sugar content similar to commercial brewing. Water, barley malt, hops, and yeast are the four main ingredients required for all-grain brewing. All-grain brewing involves a series of steps that convert the cereal starch into sugars that can be fermented by yeast that converts the sweet liquid into beer. Mashing is the process that adds heated water to ground grains, whereby enzymes present in the malted barley convert endosperm starch into fermentable sugars. Following starch conversion, heated water is added to the top of the grain mass and the sugary sweet wort is removed from the bottom (called sparging). The sweet wort is boiled and hops are added to control bitterness, flavor and aroma of the beer. The boiled wort is cooled and yeast is added. Fermentation by the yeast lasts from as short as several days to several months depending on the type of beer. When fermentation is complete the beer is bottled or put into kegs. Varying ingredients, mashing regimes and yeast type controls the type of beer brewed. Equipment for all-grain home brewing is highly variable and primarily dependent upon the monetary resources available to the brewer. All-grain brewing gives the home brewer unlimited control over the beer brewed.

### ***Correlating multiple grain measurements to grain quality.***

F.E. Dowell, E.B. Maghirang, F. Xie, and O.K. Chung.

The Grain Inspection, Packers and Stockyards Administration (GIPSA) and the Agricultural Research Service (ARS) are conducting a collaborative study to identify quantitative and qualitative tests that predict end-use traits and functionality.

We measured about 80 different traits on 100 HRWW and 100 HRSW samples selected to represent the quality range expected in the U.S. The traits measured include traditional grading factors in addition to those that measure milling, dough mixing, and baking traits. Correlation analysis of HRW quality parameters indicated that rapid tests such as protein content by NIR had a high correlation to flour water absorption (0.96), mixograph water absorption (0.96), loaf volume (0.91), farinograph absorption (0.7), kernel dimensional measurements ( $\sim -0.7$ ), and alveograph measurements (0.7–0.85). Test weight had little meaningful correlation to any parameters except to kernel dimensional characteristics ( $\sim 0.6$ ). Kernel damage as measured during grading had no correlation to any parameters, with all correlations being  $< 0.4$ . Flour yield and ash content were not well correlated to any measurements. Additional results include how combining multiple measurements improve prediction of end-use traits. This study will define how well current rapid measurement technology can predict end-use traits, and identify where improvements in rapid prediction technology may be needed.

### ***Predicting grain, flour, and bread quality using NIR spectroscopy.***

F.E. Dowell, E.B. Maghirang, F. Xie, O.K. Chung, and R.O. Pierce.

Near-infrared spectroscopy (NIRS) is used throughout the grain industry to rapidly measure characteristics of whole grain and flour, and recent research also shows that it can be used to study bread staling. We reported the accuracy of NIR and Fourier Transform (FT) NIR technology for measuring the quality of whole grain, flour, and bread. NIR and FTNIR instruments tested include the Foss 6500, Foss 1241, Perten 7200, Perten DA7000, and Cognis QTA FTNIR spectrometers. For the whole-grain analysis, we reported the accuracy of using the NIR and FTNIR instruments for measuring grain quality. We also reported the correlations of NIR and FTNIR measurements to flour quality measurements conducted on the same samples after milling. The same samples were then baked and we reported the accuracy of predicting bread quality from the NIR and FTNIR spectra collected from the flour and whole grain. The results presented in this paper should provide the grain industry with the potential and limitations of NIR and FTNIR technology for predicting grain, flour, and bread quality.

### ***Metabolites of lesser grain borer in grains.***

L.M. Seitz and M.S. Ram.

Many volatile alcohols and ester metabolites of the lesser grain borer (LGB, *Rhyzopertha dominica*) cultured on wheat grain were identified. Volatiles from infested samples at 80°C were collected on Tenax absorbent, thermally desorbed, and analyzed by gas chromatography (GC) using IR and mass (MS) detectors for component identification. A solid-phase microextraction (SPME) technique was used to analyze selected samples with a GC-MS system set up for obtaining chemical ionization mass spectra. SPME also was used in a synthesis process required to identify ester metabolites. Predominant compounds in LGB-infested grains were 2-pentanol and its esters of 2-methyl-2-pentenoic (A) and 2,4-dimethyl-2-pentenoic (B) acids, which are known aggregation pheromones, dominicalures 1 and 2. 2-Pentanol esters of saturated A,  $\beta$ -keto- and  $\beta$ -hydroxy derivatives of A and B, homologs of A and B, and acid moieties lacking the 2-Me substitution were found. Other straight- and branched-chain secondary alcohols and their esters were also observed. Reexamination of GC-MS-IR data acquired in previous investigations of LGB cultured on sorghum grain samples in a grain odor study showed the presence of many LGB metabolites in addition to the known dominicalures.

### ***Insect detection with computed tomography.***

M.D. Toews, and T.C. Pearson.

We investigated the use of computed tomography to rapidly detect kernels infested with rice weevil pupae in grain samples. Computed tomography is a medical technology that uses a computer to recreate cross sectional images of a 3-D subject from many individual x-rays. The resulting images, termed slices, were linked together to create a continuous picture of the entire grain sample. We scanned hard red winter wheat infested with rice weevil pupae at densities of 0, 5, and 10 kernels/100-g lot. A computer program was written to quickly analyze the length, width, and pixel intensity of each suspect kernel and then classify the results as number of infested kernels/100-g sample. Computer detections were

confirmed by visually inspecting each video frame. The average detection accuracy for the five infested kernels/100 g was 94.4 % with a standard deviation of 7.3 %. Similarly, the average detection accuracy in the 10 infested kernels/100 g was  $87.3 \pm 7.9$  %. Detection accuracy was slightly compromised in samples at the higher density because infested kernels were overlapping in some cases. In the control replicates, an average of  $1.2 \pm 0.92$  kernels was false positives.

### ***Detection of insect infested wheat kernels using impact acoustics.***

T.C. Pearson and D.L. Brabec.

Manual inspection of wheat kernels for insect damage is laborious, requiring approximately 20 min for a 100-g sample. Furthermore, detection of kernels with hidden damage by immature insects, before an emergence hole is created, requires slower and expensive methods, such as x-ray imaging. In this study, a method for detecting insect-damaged wheat kernels has been developed that utilizes the sound a kernel makes when it is dropped onto a steel plate. Most of the acoustic energy emitted by wheat kernels is ultrasonic, above 20 KHz and beyond what most humans can hear. Undamaged kernels tend to resonate near 40 KHz with a high initial amplitude that diminishes very quickly. In contrast, insect-damaged kernels tend to resonate below 30 KHz, have lower initial amplitudes, but resonate longer than undamaged kernels. By using signal processing methods commonly used in voice recognition technology, 90 % of the insect-damaged kernels and over 99 % of the undamaged kernels have been correctly classified. This method offers nondestructive detection and sorting of insect-infested kernels that is fast, over 40 kernels/sec (100 g in 80 sec), relatively inexpensive, accurate, and is able to detect insect-damaged kernels where the insect has not yet emerged, which will lead to more accurate estimates of insect damage in wheat loads, resulting in better flour quality.

### ***Detection of damaged wheat kernels by impact-acoustic emissions.***

T.C. Pearson, E. Cetin, A.H. Tewfik, and R.P. Haff.

A nondestructive, real time device was developed to detect insect damage, sprout damage, and scab damage in kernels of wheat. Kernels are impacted onto a steel plate and the resulting acoustic signal analyzed to detect damage. The acoustic signal was processed using four different methods: modeling of the signal in the time-domain, computing time-domain signal variances and maximums in short-time windows, analysis of the frequency spectra magnitudes, and analysis of a modified cepstrum. Features were used as inputs to a stepwise discriminant analysis routine, which selected the best subset of features for classification using a neural network. For a network presented with only insect damaged kernels (IDK) with exit holes and undamaged kernels, 87 % of the former and 98 % of the latter were correctly classified. It was also possible to distinguish undamaged, IDK, sprout-damaged, and scab-damaged kernels.

### ***Insect damage detection in wheat kernels using transmittance images.***

Z. Cataltepe, T.C. Pearson, and E. Cetin.

We used transmittance images and different learning algorithms to classify insect damaged and undamaged wheat kernels. Using the histogram of the pixels of the wheat images as the feature, and the linear model as the learning algorithm, we achieved a False Positive Rate (1-specificity) of 0.12 at the True Positive Rate (sensitivity) of 0.8 and an AUROC of  $0.90 \pm 0.02$ . Combining the linear model and a Radial Basis Function Network in a committee resulted in a FP Rate of 0.09 at the TP Rate of 0.8 and an AUC of  $0.93 \pm 0.03$ .

### ***Optical recognition of scab-damaged wheat.***

S.R. Delwiche, and T.C. Pearson.

Fusarium head blight (FHB), also known as scab, is a fungal disease that occurs in small grains. Scab results in depressed yields and can also adversely affect grain quality. Because of the potential for production of deoxynivalenol (DON), FHB is also a food safety concern. A study was conducted which examined the potential of NIR reflectance for

detection of scab-damaged wheat kernels. More than 5,000 kernels from commercial releases and breeders lines of HRSW, equally divided between infected and healthy categories, were examined by single kernel reflectance (1,000–1,700 nm). Using statistical classification techniques, such as linear discriminant analysis and nonparametric (k-nearest-neighbor) classification, an upper level for accuracy of NIR-based classification schemes at approximately 97 % was established. An exhaustive search of the most suitable wavelength pairs for the spectral difference,  $\log(1/R \text{ at wavelength } 1) - \log(1/R \text{ at wavelength } 2)$ , revealed that the low-wavelength region of a broad carbohydrate-absorption band (centered around 1,200 nm) was very effective at discriminating between healthy and scab-damaged kernels, with approximate accuracies of 95 %. Such accuracies were deemed sufficient for development of the technology for a two-wavelength high-speed commercial sorter. Ongoing research is aimed at demonstrating the reduction in DON concentration that is achieved by two-wavelength sorting.

### ***High-speed optical sorting of soft wheat for reduction of deoxynivalenol.***

S.R. Delwiche, T.C. Pearson, and D.L. Brabec.

Fusarium head blight (FHB) is a fungal disease that affects small cereal grains, such as wheat and barley, and is becoming more prevalent throughout much of the World's temperate climates. The disease poses a health risk to humans and livestock because of the associated production of the mycotoxin, deoxynivalenol (DON or vomitoxin). A study was undertaken to examine the efficiency of high-speed, optical sorting of intact wheat kernels for reduction of DON concentration. Soft red winter ( $n = 32$ ) and soft white ( $n = 3$ ) wheat samples, known to have elevated levels of FHB, were obtained from commercial mills throughout the eastern United States. An additional seven samples of wheat from the discard piles of in-mill cleaners were also studied. Fusarium-damaged wheat, cleaned of non-kernels and foreign material ( $\sim 4.5$  kg/sample, DON range = 0.6–20 mg/kg), was fed into a commercial high-speed bichromatic sorter operating at a throughput of 0.33 kg/(channel-min) and a kernel rejection rate of 10 %. A wavelength filter pair combination of 675 and 1,480 nm was selected for sorting, based on prior research. Visual measurements of the proportion of Fusarium-damaged kernels were collected on incoming and sorted (separate analyses of accepted and rejected seed), as were measurements of DON concentration. Results indicated that the fraction of DON contaminant level in the sorted wheat to that in the unsorted wheat ranged from 18 to 112 %, with an average of 51 %. Nine of the 35 regular samples and all seven of the discard pile samples underwent a second sort, with five from this second set undergoing a third sort. Multiple sorting was effective in producing wheat whose DON concentration was between 16 and 69 % of its original, unsorted value.

### ***High-speed optical sorting of soft red winter wheat for removal of Fusarium-damaged kernels.***

S.R. Delwiche, T.C. Pearson, and C.S. Gaines.

Our previous work has examined the accuracy of a semi-automated wheat scab inspection system that is based on near-infrared (NIR) reflectance (1,000–1,700 nm) of individual kernels. Classification analysis has involved the application of various statistical classification techniques, including linear discriminant analysis (LDA), soft independent modeling of class analogy (SIMCA), partial least squares (PLS) regression, and nonparametric (k-nearest-neighbor) classification. Recent research has focused on the determination of the most suitable visible or near-infrared wavelengths that could be used in high-speed sorting for removal of FHB-infected soft red winter wheat kernels. Current technology in high-speed sorters limits the number of spectral wavelengths (regions) of the detectors to no more than two. Hence, the critical aspect of this study has been the search for the single wavelengths and best two-wavelength combinations that maximize class separation, using LDA. Four thousand eight hundred kernels from 100 commercial cultivars, equally divided between normal and scab-damaged categories, were individually scanned in the extended visible (410–865 nm) and near-infrared (1,031–1,674 nm) regions. Single and all combinations of two-wavelength LDA models were developed and characterized through cross-validation by the average correctness of classification percentages. Short visible ( $\sim 420$  nm) and moderate near-infrared (1450–1500 nm) wavelengths produced the highest single-term classification accuracies (at approximately 77 % and 83 %, respectively). The best two-term models occurred near the wavelengths of 500 and 550 nm for the visible region alone (94 % accuracy), 1,152 and 1,248 nm for the near-infrared region alone (97 %), and 750 and 1,476 nm for the hybrid region (86 %). These wavelengths are, therefore, considered of importance in the design of monochromatic and bichromatic high-speed sorters for scab-damage reduction. Ongoing research is presently examining the efficiency of high-speed sorting for Fusarium-damaged kernels, as measured by reduction in DON concentration.

Approximately 40 5-kg commercial samples of SRWW have undergone as many as three successive sorts, using a commercial sorter outfitted with filters at 675 and 1,470 nm. Results indicate a significant reduction in DON is achieved through sorting; however, this comes at the expense of false positives (good kernels diverted to reject stream) and the overall reduction in material available for processing.

### ***Determining wheat vitreousness using image processing and a neural network.***

N. Wang, N. Zhang, F.E. Dowell, and T.C. Pearson.

The Grain Check 310 is a real-time, image-based wheat quality inspection machine that can replace tedious visual inspections for purity, color, and size characteristics of grains. Grain Check 310 also has the potential for measuring the vitreousness of durum wheat. Different neural network calibration models were developed to classify vitreous and non vitreous kernels and evaluated using samples from GIPSA and from fields in North Dakota. Model transferability between different inspection machines was also tested.

### ***Feasibility of summer aeration for management of wheat stored in Kansas.***

F.H. Arthur and M.E. Casada.

Temperature profiles and insect populations were compared in wheat that had been aerated with low airflow rates during the summer in addition to two autumn aeration cycles, versus wheat aerated in autumn only or unaerated. Tests were in 2000–01, 2001–02, and 2002–03, and data were analyzed separately for each year. Temperature profiles at depths of 0.9 and 1.8 m in the grain mass showed distinct declines in temperature for each aeration cycle during the first two years of the study, however, summer aeration did not result in as large of temperature declines in 2002–03, partly because the summer aerated bin was loaded with warmer grain. The effectiveness of summer aeration was estimated using confined insect populations in tube cages placed on the surface of the grain and by sampling the grain for natural insect populations using pitfall probe traps. At the conclusion of the summer aeration cycle, the number of lesser grain borer, *Rhyzopertha dominica* (Fabricius), red flour beetle, *Tribolium castaneum* (Herbst), and rice weevil, *Sitophilus oryzae* (L.) in the tube cages were consistently lower in bins that had not been aerated during the summer, possibly because without aeration temperatures in the top surface of the grain mass were high enough to limit insect populations. Pitfall trap catch of rusty grain beetles, *Cryptolestes ferrugineus* (Stephens), hairy fungus beetle, *Typhaea stercorea* (L.), foreign grain beetle, *Ahasverus advena* (Walt), and lesser grain borer was consistently lower in bins with summer aeration, indicating a reduction in natural insect populations. Field data seem to support modeling simulation studies that predict lower insect populations when a summer aeration cycle is included, however, the timing and the effectiveness of this extra aeration may vary depending on when the bins are loaded, the weather patterns for a particular year, and the presence and severity of natural infestations of insects.

### ***Grain commingling at receiving in a country elevator.***

M.E.A. Ingles, M. Casada, R.G. Maghirang, and T.J. Herrman.

The U.S. grain handling system has been developed predominantly to handle large volumes of commodity grains, and it often seems unable to preserve the identity of specialty grains to the desired level of purity. But almost no data on grain commingling during handling are available in the literature. This study evaluated commingling in a country elevator in Manhattan, Kansas. This elevator, which has a capacity of 190 t/h (7000 bu/ha), has three receiving pits and one bucket elevator leg. Experiments involved moving soybeans through one of three receiving pits followed by moving corn through the same equipment without any special cleaning between the two operations. Corn samples were collected at selected time intervals during the second operation and analyzed for commingling. Commingling was calculated as the percentage of soybean kernels mixed in the corn samples. Commingling was greater than 1 % only during the first 75 to 135 s (1 to 2 t of grain received), except for the gravity-type dump pit configuration, where commingling remained in excess of 1 % for the duration of the test (840 s or 7.3 t of grain). Measured mean cumulative commingling was 1.31 % for the combined effect of gravity-type pit and elevator leg, 0.30 % for the combined effect of leg and pit with drag conveyor, and 0.23 % for the bucket elevator alone. The effects of different receiving configurations were further

studied by using ARENA simulation with different amounts of initial impurities of incoming grains. The model predicted that a facility equipped with a bucket elevator and receiving pit with drag conveyor receiving 10 t of grain would yield to a final commingling of at least 0.28 %, of which 0.27 % would be from the effect of the leg. With minimum cleaning between loads, a load of grain handled immediately right after a load of different grain type would generate the highest amount of commingling.

### ***Heat treatment for disinfestation of empty grain storage bins.***

D.R. Tilley, M. Casada, and F.H. Arthur.

An alternative to fumigants and insecticides for controlling stored-product insects in empty grain storage bins prior to filling is heat treatment in which the temperature is quickly raised to a minimum of 50°C and held there for two to four hours. Effectiveness of heat treatments on empty grain storage bins was evaluated for five readily-available propane and electric heat treatment systems by measuring temperature and the mortality of *Tribolium castaneum* (Herbst), *Sitophilus oryzae* (L.), and *Rhyzopertha dominica* (F.) at three time intervals. Eleven locations, six above and five below the drying floor, were monitored for temperature and mortality of the three insect species using arenas initially stocked with live adult insects. Data were analyzed separately for each heating system with floor location and time interval as main effects for insect mortality. The high output propane heater (29 kW) produced 100 % mortality in 2 h for the three insect species at all test area locations. The electric duct heater system (18 kW) also produced 100 % mortality at all test area locations after 40 h when aided by a complicated interior heat distribution system. The other three systems produced less than 100 % mortality.

### ***Applications of high-speed sorting technology to the grain industry.***

F.E. Dowell and T.C. Pearson.

High speed sorters that can detect and remove defects in single kernels at speeds of about 80,000 kernels/s (300 bu/hr) are commonly used to remove undesirable product from commodities such as peanuts, tree nuts, and coffee beans. However, they have had limited use in the grain industry. We have been conducting research with Satake, Inc, with the objective of investigating grain related applications of their high-speed sorters that utilize visible and near-infrared sensors. Samples that range in size from about 100 g to 500 bu and that contain defects such as fungal damage, toxins, low or high protein, internal insects, and discolored wheat have been analyzed with this technology. Removing kernels infected with Karnal bunt with ~100 % accuracy; purifying white wheat breeder samples by removing red kernels with up to 100 % accuracy; removing low or high-protein corn from bulk samples where shifts in protein content of about 1 % can be achieved with each pass through the sorter; removing toxins such as aflatoxin and fumonisin from corn with ~90 % accuracy; and removing insect damaged kernels. This technology can be used to help breeders develop new cultivars for specific markets, to remove toxins from grain, presort grain before milling to optimize mill performance, and rapidly screen samples for grading and marketing purposes.

### ***High-throughput, grain-quality analysis.***

F.E. Dowell, T.C. Pearson, and P.R. Armstrong.

Many grain quality attributes are not uniformly distributed within the sample or bulk lot. For example, aflatoxin or fumonisin in grain may be present in only a small percentage of kernels. Our research program concentrates on developing technology or procedures to rapidly detect specific grain quality characteristics and then sort the sample or bulk-lot based on that measurement. We are working with automated single kernel systems that utilize acoustics, and color and near-infrared (NIR) sensors that can detect specific attributes and sort kernels at rates of 1 to 1,000 kernels/s. The acoustical system is being investigated for detecting insects inside single wheat kernels. The color and NIR sensors are being used to detect and remove: aflatoxin and fumonisin from corn; fumonisin from wheat; red from white wheat, red from white millet, low from high protein wheat, and damaged from undamaged corn for developing new cultivars; soft from hard wheat for studying the affects of hardness on bread quality; Karnal bunt from wheat for routine inspection; defective soybeans with off-flavors from good beans; and insect infested wheat kernels from undamaged kernels. The

lower-speed detection and sorting is based on technology developed within our research unit and commercialized by Perten Instruments, Springfield, IL. The higher-speed detection and sorting is based on electronic sorting technology developed by Satake USA Inc, Houston, Texas. This technology can help regulatory agencies rapidly screen samples; breeders develop cultivars with specific end-use traits; and researchers study specific, intrinsic kernel characteristics.

### ***Wireless data transmission of networked sensors in grain storages.***

P.R. Armstrong.

Current grain temperature monitoring systems employ sensors that are hard-wired into a structure. Thermocouples are typically used and are integrated into a supporting cable and suspended between the ceiling and floor of a structure. Multiplexed signal conditioning is performed outside the structure and the data transmitted to a display and storage device. Wireless sensors were studied as an alternative to these systems. The main issue addressed in this study was the data transmission distance that can be achieved through grain by a low power RF device designed to operate in unlicensed FCC spectrum. Results showed that sensors transmitting at 915 MHz and 1 mW power were able to communicate reliably over 2 m, although this was close to their limit. Measured signal attenuation displayed typical small-scale fading patterns, i.e. sub-wavelength changes in position caused high variability in signal strength. A 2-m range would allow reasonable spatial resolution for monitoring grain conditions such as temperature although sensors would have to be networked in order for data to be sent to an external gateway. Theory on RF attenuation in grain gave an approximation of experimental transmission signal loss but did not provide the accuracy desired to determine RF range. It was, however, helpful in selecting the most appropriate frequency range to achieve the greatest transmission distance.

### ***CO<sub>2</sub> measurement technologies and electronic noses for storage monitoring.***

P.R. Armstrong and J. Kipp.

The storage environment of grain is a micro-environment where many biological activities occur. Grain, insects, and mold produce an abundance of metabolites that could potentially be good indicators of storage conditions. Carbon dioxide has been suggested as a good indicator of bad storage conditions but is not specific to any particular problem. Various alcohols, carbonyls, and hydrocarbons have been identified as fungi volatiles, whereas volatiles specific to insects, such as aggregation pheromones dominicalure 1 and 2, and 2-pentanol, were considered to be potential problem indicators. Sensors used in electronic noses have been studied as a method to detect volatiles and determine when storage problems are caused by insects and molds. We generally thought that most sensors have the sensitivity but not the selectivity to detect many of the volatiles. We also need more research to identify the most appropriate volatiles for effective monitoring and the environmental factors under which they are formed. Carbon dioxide monitoring would seem the most promising technology for immediate application, given this sensor technology is well established.

### ***Comparison of NIR and FT-NIR spectroscopy for measuring grain and flour attributes.***

P.R. Armstrong, E.B. Maghirang, F. Xie, and F.E. Dowell.

Instruments using near-infrared reflectance (NIR) and Fourier transform near-infrared (FT-NIR) spectroscopic methods were compared for their predictive performance of several wheat flour and grain constituents. Protein, moisture, and hardness of whole grain wheat; protein, ash, and amylose of wheat flour; and corn grit fat were used to develop prediction equations between reference data of these constituents and their spectra. Partial Least Squares (PLS) regression was used to develop the prediction equations. NIR and FT-NIR spectrometers collected spectra over the wavelength ranges of 1,100–2,498 and 1,142–2,502 nm respectively. Prediction models were selected using F-test criteria ( $P = 0.05$ ). Results show that FT-NIR and NIR instruments were comparable in prediction performance and there are no apparent advantages of one over the other. Wheat flour protein and ash; whole-grain wheat protein and moisture models had good quantitative prediction based on RPD values, i.e., RPD values were greater than 5. Wheat flour amylose and whole grain wheat hardness predictions were qualitative with RPD values near 3. Corn grit fat predictions were poor with RPD values near 1.

***Accuracy of grain-moisture content prediction using temperature and relative humidity sensors.***

P.R. Armstrong, S. Uddin, and N. Zhang.

Grain temperature and moisture content (MC) are considered to be principal factors for safe storage of grain. Continuous monitoring of temperatures within grain masses is relatively easy using thermocouples, but monitoring of MC is limited by availability of sensors. However, temperature and relative humidity (RH) can be used to predict grain MC based on equilibrium moisture content (EMC) equations such as the Modified Henderson, Chung-Pfost, or Oswin. These models are limited to quasi-static thermodynamic conditions but do provide a method to predict MC with commercial sensors. Error analysis was performed using EMC relationships and temperature and RH sensor error data to determine the total error in grain MC prediction. Error inherent in the EMC regression model ( $\pm 2.15\%$  to  $\pm 3.8\%$  MC) was greater than the contribution of sensor error (approximately  $\pm 0.5\%$  to  $\pm 1\%$  MC) between storage conditions of 20–70 % RH. Outside these RH ranges, sensor error can contribute substantially ( $\pm 2\%$  to  $\pm 8\%$  MC at 95 % RH) to the total error. Development of EMC equations that exclude ranges of RH above 80 % and below 20 % may be desirable in order to develop EMC prediction equations with smaller standard errors due to regression. EMC equations respond differently to sensor error above 70 % RH, with the Oswin equation displaying the largest errors for MC prediction. Between 20 % RH and 70 % RH, there was little difference between the prediction error for the equations.

***Characterization and modeling of a high-pressure water-fogging system for grain dust control.***

D.L. Brabec, R.G. Maghirang, M.E. Casada, and E. Haque.

Grain dust, a health and safety risk, is generated whenever grain is loaded into or unloaded from hoppers and equipment. This research investigated airflow models and evaluated the particle dynamics from a high-pressure water-fog system for potential dust control at a grain-receiving hopper. A 0.2-mm (0.008-in.) spray nozzle was used to produce a plume of fog directed across a free-falling grain column. Ninety percent of the fog drops ranged from 10 to 40  $\mu\text{m}$  in diameter. Average drop velocities in the plume cross section were over 10 m/s at 7.6 cm from the nozzle. The air-velocity pressures at 7.6 cm were parabolic in the radial direction, with maximum pressures over 275 Pa (1.1 in.  $\text{H}_2\text{O}$ ). Airflow distributions, grain-dust transport, and spray-droplet trajectories within the test chamber were modeled in three dimensions using FLUENT, which is a computational fluid dynamics (CFD) software program. Induced airflow from the spray fog caused recirculation of the air and dust particles in the lower part of the chamber. This recirculation pattern transported the dust from the grain pile back into the spray plume, where it mixed with the spray fog. Experiments in a test chamber, representing a section of a grain-receiving hopper, produced side-wall fog deposits of 11  $\text{mg}/\text{cm}^2/\text{min}$  in the middle where plume and airflow was restricted by the incoming grain. The side-wall fog deposits decreased to 1.5  $\text{mg}/\text{cm}^2/\text{min}$  near the outlet. Most grain-surface fog deposits ranged from 0.1 to 0.4  $\text{mg}/\text{cm}^2/\text{sec}$ .

**Publications.**

- Alviola JN, Arora S, Lyne RK, Lookhart GL, Waniska RD, and Chung OK. 2004. Effect of dough weight and production method on wheat flour tortilla quality. National Meeting of Institute of Food Technologists/Food Expo. Book of Abstracts of the 2004 IFT Annual Meeting. Abstract (93-12). P. 242.
- Armstrong PR and Kipp J. 2004.  $\text{CO}_2$  measurement technologies and electronic noses for storage monitoring. **In:** Proc Internat Grain Quality Conf, Indianapolis, IN.
- Bechtel DB. 2004. All-grain home brewing. **In:** Program Book 89th Ann Meet AACC. Abstract 175, P. 99.
- Bechtel DB and Wilson JD. 2004. Laser diffraction sizing used to study wheat flour and starch particle size. **In:** Program Book 89th Ann Meet AACC. Abstract 21, P. 121.
- Blechl A, Chung OK, Bregitzer P, Dubcovsky J, and Sebesta P. 2004. Kernel, mixing and baking characteristics of transgenic wheats with varying HMW-GS contents. **In:** Program Book 89th Ann Meet AACC. Abstract 198, P. 103.
- Brabec DL, Maghirang RG, Casada ME, and Haque E. 2005. Characterization and modeling of a high-pressure fogging system for grain dust control. Trans ASAE (In press).
- Caley MS, Park SH, and Chung OK. 2004. A micro-baking procedure: its relation to pup straight-dough and pound sponge and dough baking methods. **In:** Program Book 89th Ann Meet AACC. Abstract 226, P. 122.
- Caltepe Z, Pearson TC, and Cetin AE. 2005. Insect damage detection in wheat kernels using transmittance images. Proceedings of the IEEE International Conference on Image Processing (ICIP). Cereal Chem (In review).

- Chung OK. 2003. Characterization of cereals and flours (Kaletunc G and Breslauer KJ, Eds). Marcel Dekker, Inc., New York. 15:119-120.
- Chung OK. 2004. How wheat breeding brings benefits for users and consumers. **In:** Program Book 89th Ann Meet AACC. Abstract 139, P. 91.
- Chung OK, Gaines CS, Morris CF, and Hareland GA. 2004. Roles of the four ARS regional wheat quality laboratories in U.S. wheat quality improvement. **In:** Proc 12th ICC Internat Cereal and Bread Cong, 23-26 May, 2004, Harrogate, UK. Pp. 1-5 (CD version).
- Chung OK, Lookhart GL, Dowell FE, Tilley M, Bean SR, Seitz LM, Seabourn BW, Park SH, Steele JL, Casada ME, Ram MS, Maghirang EB, Pasikatan MC, Kim YS, Bechtel DB, Perez-Mendoza J, Xie F, Lyne RK, Singh H, Caley MS, Wilson JD, Brabec DL, Ohm JB, Throne JE, Baker JE, Pearson TC, and Haden ZL. 2004. Wheat research in the U.S. Grain Marketing Research Laboratory, GMPRC, USDA-ARS. Ann Wheat Newslet 50:221-238.
- Chung OK, Maghirang EB, Park SH, Caley MS, Dowell FE, and Seabourn BW. 2004. Quality parameters of four wheat fractions singulated and sorted based on kernel hardness. **In:** Program Book 89th Ann Meet AACC. Abstract 417, P. 167.
- Chung OK and Park SH. 2004. A comparison of a farinograph (10-g flour) with variable mixing speed to a mixograph (10-g flour) in flour testing. **In:** Program Book 89th Ann Meet AACC. Abstract 360, P. 154.
- Delwiche SR and Pearson TC. 2004. Optical recognition of scab-damaged wheat. **In:** Program Book 89th Ann Meet AACC. Abstract.
- Delwiche SR, Pearson TC, and Gaines CS. 2004. High-speed optical sorting of soft red winter wheat for removal of fusarium-damaged kernels. **In:** Program Book 89th Ann Meet AACC. Abstract.
- Don C, Lookhart GL, Naeem H, MacRitchie F, and Hamer RJ. 2004. Glutenin particles are affected by growing conditions. **In:** Proc Internat Gluten Workshop.
- Don C, Lookhart GL, Naeem H, MacRitchie F, and Hamer RJ. 2004. The effect of wheat genetic background and growing conditions on the glutenin macro-polymer. J Cereal Sci (In press).
- Dowell FE, Maghirang EB, Xie F, and Chung OK. 2004. Correlating multiple grain measurements to grain quality. **In:** Program Book 89th Ann Meet AACC. Abstract.
- Dowell FE, Maghirang EB, Xie F, Chung OK, and Pierce RO. 2004. Predicting grain, flour, and bread quality using NIR spectroscopy. **In:** Proc Internat Cereal and Bread Cong, Harrogate, England. 23-24 May, 2004.
- Dowell FE and Pearson TC. 2004. Applications of high-speed sorting technology to the grain industry. **In:** Program Book 89th Ann Meet AACC. Abstract.
- Dowell FE, Pearson TC, and Armstrong PR. 2004. High throughput grain quality analysis. Presented at the AOAC International Annual Meeting, St. Louis, Mo, 19-23 September.
- Graybosch RA, Peterson CJ, and Chung OK. 2004. Registration of N95L11881 and 97L9521 strong gluten 1BL·1RS wheat germplasm lines. Crop Sci 44:1490-1491.
- Graybosch RA, Peterson CJ, Porter DR, and Chung OK. 2004. Registration of N96L9970 Greenbug resistant wheat. Crop Sci 44:1492-1493.
- Graybosch RA, Souza EJ, Berzonsky WA, Baenziger PS, McVey DJ, and Chung OK. 2004. Registration of nineteen waxy spring wheats. Crop Sci 44:1491-1492.
- Haley SD, Johnson JJ, Peairs FB, Westra PW, Quick JS, Stromberger JA, Clayshulte SR, Clifford BL, Rudolph JB, Seabourn BW, and Chung OK. 2004. Registration of 'Protection' wheat. Crop Sci (In review).
- Haley SD, Quick JS, Peairs FB, Johnson JJ, Stromberger JA, Clayshulte SR, Clayshulte SR, Clifford BL, Rudolph JB, Seabourn BW, Chung OK. 2005. Registration of 'Hatcher' wheat. Crop Sci (In press).
- Haley SD, Quick JS, Johnson JJ, Peairs FB, Stromberger JA, Clayshulte SR, Clifford BL, Rudolph JB, Chung OK, and Seabourn BW. 2004. Registration of 'Anchor' wheat. Crop Sci 44:1025-1026.
- Haley SD, Quick JS, Peairs FB, Johnson JJ, Westra J, Stromberger JA, Clayshulte SR, Clifford BL, Rudolph JB, Seabourn BW, and Chung OK. 2005. Registration of 'Bond CL' wheat. Crop Sci (In press).
- Hubbard JD, Downing JD, Ram MS, and Chung OK. 2004. Lipid extraction from wheat flour using supercritical fluid extraction. Cereal Chem 81:693-698.
- Ibrahim AMH, Haley SD, Jin Y, Langham MAC, Stymiest C, Rickertsen J, Kalsbeck S, Little R, Chung OK, Seabourn BW, and McVey DV. 2004. Registration of 'Expedition' Wheat. Crop Sci 44:1470-1471.
- Ingles MEA, Casada M, Maghirang RG, and Herrman TJ. 2004. Grain commingling at receiving in a country elevator. **In:** Proc Internat Quality Grains Conf, Indianapolis, IN.
- Jones BL and Lookhart GL. 2004. Comparison of the endoproteinases of various grains. Cereal Chem (In press).
- Lookhart GL and Bean SR. 2004. Capillary electrophoresis of cereal proteins: an overview. J Capillary Electrophoresis (In press).

- Lookhart GL, Bean SR, and Culbertson CT. 2004. Wheat quality and wheat varietal identification. **In:** Internat Assoc for Cereal Sci Tech Jubilee Conf Proc (In press).
- Park SH, Chung OK, and Seib PA. 2004. Effects of varying weight ratios of large and small wheat starch granules on experimental straight dough bread. *Cereal Chem* (In press).
- Park SH, Chung OK, and Seib PA. 2004. Size distribution and properties of wheat starch granules in relation to crumb grain score of pup-loaf bread. *Cereal Chem* 81:699-704.
- Pearson TC and Brabec DL. 2005. Detection of insect infested wheat kernels using impact acoustics. **In:** Program Book 89th Ann Meet AACC. Abstract.
- Ram MS and Chung OK. 2004. Sequential extraction of nonpolar and polar classes of wheat flour lipids using supercritical-CO<sub>2</sub> with ethanol modifier. **In:** Program Book 89th Ann Meet AACC. Abstract 222, P. 121.
- Ram MS and Chung OK. 2004. Wheat flour lipids extracted by a dual-pump CO<sub>2</sub>-ethanol supercritical fluid extraction system. **In:** Prog Book 11th Internat Symp and Exhibit on Supercritical Fluid Chromatography, Extraction, and Processing, Pittsburgh, PA, 1-4 August, 2004. Abstract A-01, P. 160.
- Ram MS, Seitz LM, and Dowell FE. 2004. Natural fluorescence of red and white wheat. *Cereal Chem* 81:244-248.
- Reamer E, Tilley M, Srivarin P, and Tilley KA. 2004. Changes in tyrosine, dityrosine and phosphotyrosine content in wheat varieties exposed to heat stress. **In:** Program Book 89th Ann Meet AACC. Abstract, P. 151.
- Seabourn BW, Bean SR, Park SH, Lookhart GL, and Chung OK. 2004. Prediction of polymeric protein content in wheat flour by NIR. *Cereal Chem* (In review).
- Seabourn BW, Xie F, and Chung OK. 2004. Rapid determination of dough-mixing requirement for early generation breeding lines by FT-HATR mid-infrared spectroscopy. **In:** Program Book 89th Ann Meet AACC. Abstract 368. Pp. 155-156.
- Seibel W, Chung OK, Weipert D, and Park SH. 2005. Cereal and Cereal Products. *Ullmann Encyclopedia* (CD format) (In review).
- Seitz LM and Ram MS. 2004. Metabolites of lesser grain borer in grains. *J Agric and Food Chem* 52:898-908.
- Singh H, Lyne RK, Chung OK, Park SH, and Lookhart GL. 2004. Correlation of wheat protein composition and dough rheological properties to tortilla quality. **In:** Program Book 89th Ann Meet AACC. Abstract 394, P. 162.
- Tilley M. 2004. PCR amplification of wheat<sup>o</sup>sequences from DNA extracted during milling and baking. *Cereal Chem* 81:44-47.
- Tilley M and Tilley KA. 2004. Modifying crosslink formation in wheat dough by controlling innate enzyme activity. **In:** Program Book 89th Ann Meet AACC. Abstract.
- Toews MD and Pearson TC. 2004. Insect detection with computed tomography. 2004 USDA-CSREES-RAMP Project Meeting, Salt Lake City, UT, 13 November.
- Waniska RD, Cepeda M, King BS, Adams JL, Rooney LW, Torres PI, Lookhart GL, Bean S, Wilson JD, and Bechtel DB. 2004. Effects of flour properties on tortilla quality. *Cereal Foods World* 49:237-244.
- Wilson JD and Bechtel DB. 2004. Measuring wheat starch size distribution using image analysis and laser diffraction technology. **In:** Program Book 89th Ann Meet AACC. Abstract.
- Xiao SZ, Park SH, and Chung OK. 2005. Testing four solvents for solvent retention capacity (SRC) in hard winter wheat flour and their use in a regression equation to predict bread loaf volume. **In:** Program Book 89th Ann Meet AACC. Abstract 224, P. 122.

**MINNESOTA**

**CEREAL DISEASE LABORATORY, USDA—ARS**  
**University of Minnesota, 1551 Lindig St., St. Paul, MN 55108, USA.**  
**www.cdl.umn.edu**

D.L. Long, J.A. Kolmer, Y. Jin, M.E. Hughes, and L.A. Wanschura.

### *Wheat rusts in the United States in 2004.*

**Wheat stem rust** (*Puccinia graminis* f. sp. *tritici*). The first reports of wheat stem rust in 2004 were in late April, when trace levels of infection were found in plots at Giddings in central Texas and at Quincy in the Florida panhandle. The next report of wheat stem rust was in early June, when trace to 5% severities were reported in a wheat breeding nursery in northeastern Kansas. In early June, traces of wheat stem rust were found in an experimental line in a nursery in northeastern Missouri.

In late June, severe stem rust was observed in plots of the susceptible cultivar Red Chief at Lincoln, NE. In late June, traces of stem rust were found in a field of triticale in southeastern Minnesota, which is in the same area where barberry bushes occur. The stem rust found on triticale was determined to be rye stem rust.

In the first week of July, trace levels of stem rust infections were found on the susceptible spring wheat Baart in southern Minnesota. By mid-July, 20–60 % severities were observed on Baart in central Minnesota and central South Dakota plots. All of the current spring wheat cultivars are resistant to the current race population. In susceptible winter wheat plots in east central Minnesota, trace to 60 % severities were found at the soft dough growth stage. In mid-July, traces of wheat stem rust were found on winter wheat in west central Wisconsin. In late July, trace to 20 % severities were observed on the susceptible spring wheat Baart in central North Dakota and north central Minnesota.

From April to June, there were very few reports of wheat stem rust being found in the southern and central plains. However, in July stem rust was present on susceptible cultivars at many locations from western Wisconsin to central North Dakota. Therefore, the stem rust that developed throughout the north must have originated from the few inoculum sources in the southern and central plains.

Race QFCS, the predominant race found in the Great Plains the past few years, was again the predominant race identified in 2004 (Table 1). The majority of wheat varieties in the United States are resistant to race QFCS. Races MCC and TPMK were found at localities where field inoculation was used in the screening nurseries. Race QCCN, a race similar to QCCJ in virulence, was identified from a collection from Washington.

**Table 1.** Races of *Puccinia graminis* f. sp. *tritici* identified from wheat in 2004. Pgt race code after Roelfs and Martens (Phytopathology 78:526-533). Race QFCS virulent to *Sr5*, *Sr8a*, *Sr9a*, *Sr9d*, *Sr9g*, *Sr10*, *Sr17*, and *Sr21*; MCCF virulent to *Sr5*, *Sr7d*, *Sr9g*, *Sr10*, *Sr17*, and *SrTmp*; MCCD virulent to *Sr5*, *Sr7d*, *Sr9g*, *Sr10*, and *Sr17*; TPMK virulent to *Sr5*, *Sr7b*, *Sr8a*, *Sr9d*, *Sr9e*, *Sr9g*, *Sr10*, *Sr11*, *Sr17*, *Sr21*, *Sr36*, and *SrTmp*; and QCCN virulent to *Sr5*, *Sr9a*, *Sr9g*, *Sr10*, *Sr17*, and *Sr21*. Set four consists of *Sr9a*, *Sr9d*, *Sr10*, and *SrTmp*.

Area	State	Collections	Isolates	Number of isolates of Pgt- race				
				QFCS	MCCF	MCCD	TPMK	QCCN
Great Plains	TX	1	1	1				
	OK	1	1	1				
	KS	3	3	3				
	NE	3	2	1			1	
	SD	3	3	3				
	ND	7	6	6				
Midwest	MO	1	1	1				
	IN	1	1		1			
	MN	15	19	15	2	2		
Pacific NW	WA	1	2					2
U.S. Total		36	39	31	3	2	1	2

**Wheat leaf rust (*Puccinia triticina*). Southern Plains.** In late January, traces of leaf rust were found in central Texas plots. Cool temperatures during early February slowed leaf rust development. By late February, 40 % leaf rust severities were observed in central Texas plots. In the second week of March, 60 % leaf rust severities were reported on susceptible cultivars in southern Texas (east of San Antonio). Leaf rust was scattered and severe in more places throughout Texas than in 2003.

By early March, leaf rust was present in Oklahoma but at lower severity levels than in the previous autumn. In 2004, cold temperatures during mid-January to mid-February were not conducive for over wintering of rust in Oklahoma.

In late March, in southern and central Texas, leaf rust infections were at low severity levels in most commercial wheat fields (Fig. 1) and at high severity levels on susceptible cultivars in nursery plots. Leaf rust severities up to 80 % were found on lower leaves of cultivars in nurseries, and trace–20 % severity levels were on lower leaves in fields. Rainfall in mid to late March contributed to the leaf rust development in the southern Great Plains.

In mid-April, leaf rust was found from Texas to Kansas. In most of southern and central Texas, rain and dew periods were ideal for the infection process to occur. In a central Texas nursery on the susceptible cultivar Jagger, the leaves were completely dead due to heavy rust infections.

In late April in central Texas, susceptible cultivars had moderate to high severities of rust infection, whereas in northern Texas, susceptible cultivars had light to moderate leaf rust infection. In central Texas fields, 40 % severities were observed in fields that had been sprayed with fungicide (Fig. 1). By early May, leaf rust was increasing throughout Oklahoma, but drier than normal conditions in mid-May significantly slowed rust development. As in previous years, Jagger wheat was heavily rusted and some yield reduction occurred. Leaf rust in the southern Great Plains was more severe than 2003, but dry conditions in some areas slowed rust development.

**Central Plains.** In early April, traces of leaf rust were found in several fields in south central Kansas. In early May,

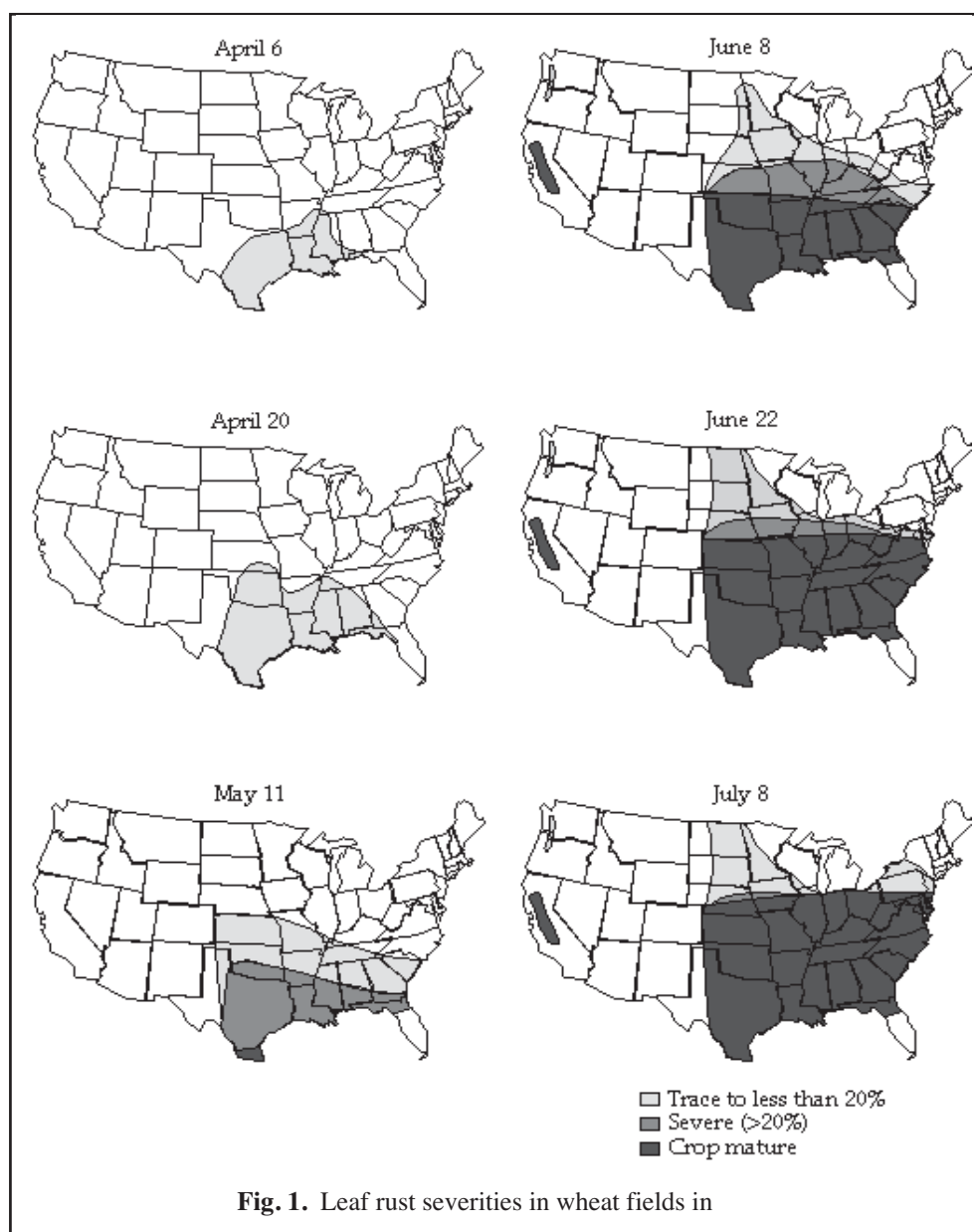


Fig. 1. Leaf rust severities in wheat fields in

leaf rust was present in most of Kansas at trace severities except in south central Kansas where 10 % severities were reported on lower leaves in some fields. By the third week in May, leaf rust was starting to increase on flag leaves in south central Kansas.

In the last week in May, leaf rust was severe in plots and fields of susceptible cultivars from north central Kansas to west central Missouri (Fig 1, p. 212). At the late berry stage in south central Kansas, Jagger had 60 % rust severities on flag leaves while in northeast Kansas, Jagger had 20 % rust severities. In central Kansas varietal plots, rust severities ranged from trace to 80 %. In southern Kansas, losses due to leaf rust were severe in Jagger, whereas other leaf rust susceptible cultivars had lower yield losses (Table 4). Rainfall in late May, in Kansas and Nebraska allowed leaf rust to increase which provided inoculum for the northern wheat growing area.

In mid June, leaf rust was severe in southeast and south central Nebraska (Fig. 1). Rust severities on flag leaves were 60 to 80% in fields and experimental plots. Abundant rainfall in eastern and southern Nebraska provided good moisture conditions for rapid increase of leaf rust infections. In western Nebraska where it was much dryer, only trace levels of leaf rust infections were observed (Table 4, p. 217).

**Northern Plains.** In early June, trace amounts of leaf rust were found on winter wheat lines in plots at Brookings in east central South Dakota.

In early June, trace levels of leaf rust were found in winter wheat plots in east central Minnesota. Traces of leaf rust infections were also found in spring wheat in the Red River Valley in early June. In mid-June, leaf rust was increasing in winter wheat in southeastern South Dakota and southern Minnesota, with severities of 20–40 % on lower leaves and 10–20 % on flag leaves. The spring wheat crop had trace to 5 % levels of infections on lower leaves. In mid-June in an east central South Dakota rust nursery, high levels of leaf rust were observed on the susceptible spring wheat cultivars Thatcher, Baart, and Morocco. During the second week in June, traces of leaf rust were found in fields in southeast and north central North Dakota. Rainfall and cool-warm temperatures provided suitable conditions for the increase and spread of leaf rust in the north central region.

In early July in east central Minnesota plots, susceptible winter wheat cultivars such as Jagger had 80 % rust severities, but the resistant cultivars had only trace levels of infections on the flag leaves. The leaf rust did not over winter in the Minnesota plots, but probably originated from field infections in Oklahoma and Kansas.

In early July, susceptible spring wheat cultivars in southern Minnesota plots had 20 % rust severities, with most infections on the lower leaves. Trace levels of leaf rust were observed in many of the spring wheat fields in southern Minnesota (Fig. 1). In the first week of July, leaf rust severities were up to 80 % on susceptible spring wheat cultivars such as Ingot in southern and west central Minnesota varietal plots. The spring wheat Oxen, which is commonly grown in southern Minnesota, had leaf rust severities of 30–60 %; the cultivar Alsen had leaf rust severities of 5–10 % in southern and west central Minnesota.

In mid-July, 10–40 % leaf rust severities were observed on flag leaves of spring wheat cultivars in fields from northwestern South Dakota to northeastern Wisconsin.

In late July, spring wheat varietal plots had trace to 60 % leaf rust severities in central and eastern North Dakota. Fields in southeastern and central North Dakota of commonly grown wheat cultivars had severity levels of 20 %. Many wheat fields were sprayed with fungicide to prevent losses due to rust and scab. In the northern tier of counties in North Dakota leaf rust was at reduced levels because the crop maturity was later than normal.

This year leaf rust was severe and concentrated in the upper Midwest. Rust inoculum arrived from the south in late May and early June with rain showers while temperature and moisture conditions were good for infection and spread of leaf rust. The spring wheat cultivars currently grown have less effective resistance to leaf rust than those that were popular 10–15 years ago. Losses to wheat leaf rust occurred in cultivars that had not been sprayed with fungicide. In 2004, a 10 % loss in the spring wheats to leaf rust was determined in Minnesota (Table 4, p. 217).

**Southeast.** In mid-January, leaf rust was reported in southwest Louisiana. By early March, leaf rust was at significant severity levels in south/west central Louisiana. Rust was widespread and severities of 30 % were in nursery plots and fields. Some cultivars had heavy rust severities on older leaves (fall infection), but low severities on the upper leaves.

In mid-February, fields and plots in Baldwin County in southwest Alabama had low severities of leaf rust. In late February weather conditions were ideal for further rust development in the southeastern U.S.

In late March, leaf rust was present in fields and plots in the southern soft red winter wheat area from Georgia to Arkansas. Some of the fields infected with rust were sprayed for rust control.

In mid-April from central Louisiana through Alabama to Georgia, low levels of leaf rust infection were observed in research plots and fields. On a few susceptible cultivars 40 % severities were reported in south central Louisiana nurseries. In early May, plots from central Texas to the Florida Panhandle had 80 % leaf rust severities.

By mid-April, leaf rust was increasing in areas of Arkansas that had sufficient moisture. In late April, light to moderate leaf rust was in Arkansas fields and plots. In early May nursery plots in northwestern Arkansas had 50 % rust severities. In mid-May, leaf rust was prevalent throughout Arkansas, but rust infections developed later than normal and did not cause much yield loss (Table 4, p. 217).

**Midwest.** In late May, susceptible cultivars had 20–25 % leaf rust severities at the late milk stage in southwest Indiana wheat plots. This was the most leaf rust seen in a number of years in this area. In early June, plots in west central Indiana had 20 % severities while traces were found in fields.

In early June, leaf rust developed late in central Ohio and susceptible cultivars had 20 % severities on flag leaves, which resulted in losses. During the second week in June, trace to 10 % severities was found in plots in northwest Ohio, northern Indiana and south central Wisconsin. Only light losses occurred in this area (Table 4).

**East.** In late May, hot, dry weather hastened the maturity of small grains in the Carolinas and Virginia. Powdery mildew was widespread on wheat and in some fields appeared to be at damaging levels. Leaf rust on winter wheat was either nonexistent or very light in commercial fields. In nursery plots in eastern North Carolina, leaf rust was severe only on fully susceptible cultivars.

In eastern Virginia, the wheat crop matured 10 days earlier than normal because of the hot temperatures in May, which halted the leaf rust development. In early June in western Virginia, the crop matured at a normal pace and more leaf rust was found there. Varieties with *Lr26*, e.g., USG 3209 and Sisson, had considerable leaf rust. In early June, moderate to light levels of leaf rust infection were observed in winter wheat plots in central Maryland.

In early July, wheat leaf rust was widespread, but not severe throughout western and central New York.

**California.** Wheat leaf rust was late to develop and was only found on a few cultivars. The wheat crop matured early and leaf rust did not affect the yield.

**Pacific Northwest.** In late May, trace amounts of leaf rust were observed in wheat plots and fields in northwest Washington. In early June, severe leaf rust was reported in the Willamette Valley in northwest Oregon.

In late June, foci of 20 % leaf rust severity were found in soft white winter wheat plots in northeastern Oregon at Pendleton. Leaf rust development was light in the Pacific Northwest this year.

**Canada.** In mid-June, traces levels of leaf rust were found in winter wheat plots south of Winnipeg, Manitoba, Canada.

**Wheat leaf rust virulence.** The 2004 leaf rust race identifications are presented in Table 2 (p. 215) and Table 3 (p. 216) (see Fig. 2, p. 216, for agroecological area map). A total of 50 leaf rust races were found in the U.S. From the central and southern Plains the most common races were M— (virulent to *Lr1*, *Lr3*, *Lr10*, and *Lr17*) (Table 3). Many of the MBDS and MCDS races were identified from collections made from Jagger, which is widely grown in the southern and central Plains states. The number of T-races (TNRJ and TNBJ) with virulence to *Lr9*, *Lr10*, and *Lr24* in collections made from the cultivars Lockett (*Lr9* resistance) and Thunderbolt (*Lr41* resistance) has increased. In 2004, the most common races identified in the northern wheat growing area were T-races (TBBJ, TBDS, and TCDS). At the same time, there was an increase in the number of K-races (virulent to *Lr2a*, *Lr2c*, and *Lr3*) (Table 2). In the soft red wheat area the most common race was MCRK (virulent to *Lr1*, *Lr3*, *Lr3ka*, *Lr10*, *Lr11*, *Lr14a*, *Lr18*, *Lr26*, and *Lr30*). Some of the commonly grown cultivars in this area have *Lr11* and *Lr26* resistance.

**Table 2.** Races of *Puccinia triticina* in the U.S. in 2004 determined by virulence to 16 near-isogenic lines of Thatcher wheat with leaf rust-resistance genes. Area 1 includes the U.S. states of AL, AR, FL, GA, LA, MS, NC, and SC; Area 2, DE, MD, NJ, NY, PA, VA, and WV; Area 3, IL, IN, KY, MI, MO, OH, TN, and WI; Area 4, NM, OK, and TX; Area 5, CO, IA, KS, and NE; Area 6, MN, MT, ND, SD, and WY; Area 7, CA, and UT; and Area 8, ID, OR, and WA (See Fig. 2). Differentials used: 1,2a,2c,3,9,16,24,26,3ka,11,17,30,B,10,14a,18. An \* indicates less than 0.6 %.

Race	Virulence combination (ineffective <i>Lr</i> genes)	Area 1		Area 2		Area 3		Area 4		Area 5		Area 6		Area 7		Area 8		U.S. Total	
		#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
BBBD	14a	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0.3
BBBG	10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	17	2	0.3
CBBG	3,10	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0.1
CLDS	3,9,17,B,10,14a,	0	0	0	0	0	0	2	1	1	1	0	0	0	0	0	0	3	0.4
KBBG	2a,2c,3,10	0	0	0	0	1	2	6	3	5	3	63	26	0	0	1	8	76	10.0
KBBJ	2a,2c,3,10,14a	0	0	0	0	0	0	4	2	4	2	9	4	0	0	0	0	17	2.2
KCBJ	2a,2c,3,26,10,14a	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0.3
KDBG	2a,2c,3,24,10	0	0	0	0	0	0	8	5	4	2	2	1	0	0	0	0	14	1.8
KDBJ	2a,2c,3,24,10,14a	0	0	0	0	0	0	0	0	4	2	0	0	0	0	0	0	4	0.5
KDDG	2a,2c,3,24,17,10	0	0	0	0	0	0	4	2	0	0	0	0	0	0	0	0	4	0.5
KDDJ	2a,2c,3,24,17,10,14a	0	0	0	0	0	0	4	5	0	0	0	0	0	0	0	0	4	0.5
KFBJ	2a,2c,3,24,26,10,14a	0	0	0	0	0	0	0	0	3	2	0	0	0	0	0	0	3	0.4
KGBG	2a,2c,3,16,10	0	0	0	0	1	2	0	0	2	1	11	5	0	0	0	0	14	1.8
KGBJ	2a,2c,3,16,10,14a	0	0	0	0	0	0	0	0	3	1	8	3	0	0	0	0	11	1.4
KJBJ	2a,2c,3,16,24,10,14a	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	1	0.1
MBDS	1,3,17,B,10,14a	7	7	1	7	5	12	32	18	16	9	15	6	0	0	3	25	79	10.4
MBGJ	1,3,11,10,14a	2	2	0	0	4	10	0	0	0	0	0	0	0	0	0	0	6	0.8
MBRJ	1,3,3ka,11,30,10,14a	0	0	0	0	0	0	0	0	1	1	*	0	0	0	0	0	2	0.3
MBRK	1,3,3ka,11,30,10,14a,18	2	2	0	0	1	2	2	1	0	0	0	0	0	0	0	0	5	0.7
MCDS	1,3,26,17,B,10,14a	3	3	4	29	21	50	15	9	21	12	32	13	2	67	3	25	102	13.4
MCRK	1,3,26,3ka,11,30,10,14a,18	29	29	3	21	2	5	0	0	2	1	0	0	0	0	0	0	36	4.7
MDBJ	1,3,24,10,14a	1	1	0	0	0	0	5	3	2	1	2	1	0	0	0	0	10	1.3
MDDS	1,3,24,17,B,10,14a	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	2	0.3
MFBJ	1,3,24,26,10,14a	0	0	0	0	2	5	0	0	0	0	0	0	0	0	0	0	2	0.3
MFDS	1,3,24,26,17,B,10,14a	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
MHDS	1,3,9,16,26,17,B,10,14a	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	8	1	0.1
MLDS	1,3,9,17,B,10,14a	0	0	0	0	0	0	13	7	3	2	2	1	0	0	0	0	18	2.4
SBDD	1,2a,2c,17,14a	0	0	0	0	0	0	0	0	0	0	1	*	0	0	0	0	1	0.1
TBBF	1,2a,2c,3,14a,18	0	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	1	0.1
TBBG	1,2a,2c,3,10	0	0	0	0	0	0	2	1	0	0	2	1	0	0	2	17	6.	0.8
TBBJ	1,2a,2c,3,10,14a	8	8	0	0	0	0	16	9	15	9	7	3	0	0	0	0	46	6.0
TBDS	1,2a,2c,3,17,B,10,14a	2	2	0	0	0	0	5	3	21	12	17	7	0	0	0	0	45	5.9
TBRJ	1,2a,2c,3,3ka,11,30,10,14a	0	0	0	0	0	0	3	2	0	0	0	0	0	0	0	0	3	0.4
TBTJ	1,2a,2c,3,3ka,11,17,30,10,14a	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	2	0.3
TCBJ	1,2a,2c,3,26,10,14a	0	0	2	14	0	0	0	0	10	6	0	0	0	0	0	0	12	1.6
TCDS	1,2a,2c,3,26,17,B,10,14a	4	4	4	29	2	5	0	0	28	16	13	5	0	0	0	0	51	6.7
TCGJ	1,2a,2c,3,26,11,10,14a	7	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	0.9
TCRK	1,2a,2c,3,26,3ka,11,30,10,14a,18	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0.5
TCTB	1,2a,2c,3,26,3ka,11,17,30	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0.3
TCTD	1,2a,2c,3,26,3ka,11,17,30,14a	4	4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0.5
TCTG	1,2a,2c,3,26,3ka,11,17,30,10	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0.4
TDBJ	1,2a,2c,3,24,10,14a	0	0	0	0	0	0	6	3	1	1	0	0	0	0	0	0	7	0.9
TDDS	1,2a,2c,3,24,17,B,10,14a	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	1	0.1
TGBJ	1,2a,2c,3,16,10,14a	1	1	0	0	0	0	0	0	0	0	5	2	0	0	0	0	6	0.8
THBJ	1,2a,2c,3,16,26,10,14a	2	2	0	0	0	0	8	5	3	2	17	7	0	0	0	0	30	3.9
TJBJ	1,2a,2c,3,16,24,10,14a	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	2	0.3
TLGJ	1,2a,2c,3,9,11,10,14a	10	10	0	0	1	2	6	3	0	0	2	1	0	0	0	0	19	2.5
TLRJ	1,2a,2c,3,9,3ka,11,30,10,14a	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	2	0.3
TNBJ	1,2a,2c,3,9,24,10,14a	2	2	0	0	0	0	0	0	4	2	2	1	1	33	0	0	9	1.2
TNRJ	1,2a,2c,3,9,24,3ka,11,30,10,14a	5	5	0	0	0	0	32	18	13	8	27	11	0	0	0	0	77	10.1
Total		101		14		42		177		172		242		3		12		763	

**Wheat stripe rust (*Puccinia striiformis* f. sp. *tritici*). Southern Plains.** In late February, severe wheat stripe rust was found in plots southwest of Houston, Texas. By the second week in March, the stripe rust development in these plots had stopped. In mid-March, there were reports of stripe rust in fields west of Brazos and Williamson counties in central Texas.

**Table 3.** Virulence frequencies (%) of *Puccinia triticina* in the U.S. in 2004 to 16 differential lines of Thatcher wheat with leaf rust resistance genes. Area 1 includes the U.S. states of AL, AR, FL, GA, LA, MS, NC, and SC; Area 2, DE, MD, NJ, NY, PA, VA, and WV; Area 3, IL, IN, KY, MI, MO, OH, TN, and WI; Area 4, NM, OK, and TX; Area 5, CO, IA, KS, and NE; Area 6, MN, MT, ND, SD, and WY; Area 7, CA, and UT; and Area 8, ID, OR, and WA (See Fig. 2)

Resistance gene	Area 1		Area 2		Area 3		Area 4		Area 5		Area 6		Area 7		Area 8		U.S. Total	
	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%	#	%
<i>Lr1</i>	100	99.0	14	100.0	39	92.9	149	84.2	142	82.6	149	61.6	3	100.0	9	75.0	605	79.3
<i>Lr2a</i>	54	53.2	6	42.9	7	16.7	107	60.5	122	70.9	190	78.5	1	33.3	3	25.0	490	64.2
<i>Lr2c</i>	54	53.2	6	42.9	7	16.7	107	60.5	122	70.9	190	78.5	1	33.3	3	25.0	490	64.2
<i>Lr3</i>	101	100.0	14	100.0	42	100.0	177	100.0	170	98.8	241	99.6	3	100.0	10	83.3	758	99.3
<i>Lr9</i>	17	16.8	0	0.0	1	2.4	55	31.1	21	12.2	33	13.6	1	33.3	0	0.0	128	16.8
<i>Lr16</i>	3	3.0	0	0.0	2	4.8	8	4.5	8	4.7	43	17.8	0	0.0	1	8.3	65	8.5
<i>Lr24</i>	10	9.9	0	0.0	3	7.1	60	33.9	33	19.2	35	14.5	1	33.3	0	0.0	142	18.6
<i>Lr26</i>	60	59.4	13	92.9	27	64.3	24	13.6	69	40.1	62	25.6	2	66.7	4	33.3	261	34.2
<i>Lr3ka</i>	49	48.5	3	21.4	3	7.1	39	22.0	16	9.3	30	12.4	0	0.0	0	0.0	140	18.3
<i>Lr11</i>	68	67.3	3	21.4	8	19.0	45	25.4	16	9.3	32	13.2	0	0.0	0	0.0	172	22.5
<i>Lr17</i>	27	26.7	9	64.3	28	66.7	77	43.5	92	53.5	82	33.9	2	66.7	7	58.3	324	42.5
<i>Lr30</i>	49	48.5	3	21.4	3	7.1	39	22.0	16	9.3	30	12.4	0	0.0	0	0.0	140	18.3
<i>LrB</i>	18	17.8	9	64.3	28	66.7	69	39.0	92	53.5	79	32.6	2	66.7	7	58.3	304	39.8
<i>Lr10</i>	95	94.1	14	100.0	41	97.6	177	100.0	170	98.8	241	99.6	3	100.0	12	100.0	753	98.7
<i>Lr14a</i>	95	94.1	14	100.0	40	95.2	157	88.7	161	93.6	164	67.8	3	100.0	7	58.3	641	84.0
<i>Lr18</i>	35	34.7	3	21.4	4	9.5	2	1.1	2	1.2	0	0	0	0.0	0	0.0	46	6.0
Total	101		14		42		177		172		242		3		12		763	

In late March, wheat stripe rust infections were at low levels in fields in southern and central Texas (Fig 3, p. 218). Stripe rust severities ranged from trace levels to 20 % in plots and fields. Although rainfall in late March provided high moisture conditions, warmer day and night temperatures restricted stripe rust development. In mid-April, stripe rust was light in southern and central Texas.

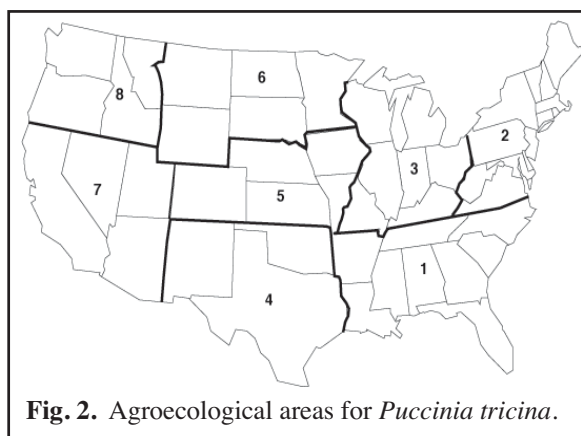
In late April, stripe rust was light to moderate in north central Texas and southern Oklahoma plots and fields (Fig. 3, p. 218). In north central Texas, 60 % severities were observed on susceptible varieties. Some fields in this area had been sprayed for rust and mildew control. In early May, stripe rust was found across northern Oklahoma. Rust was present in significant amounts, but dry and windy conditions impeded the further development of stripe rust on susceptible cultivars. Hot spots of rust development were found in central and southwestern Oklahoma, but not at levels that caused significant yield losses (Table 4, p. 217).

This year stripe rust was found in fewer locations and the weather conditions were not as conducive for stripe rust development as 2003 in Texas and Oklahoma. Another possibility is that stripe rust over wintering was reduced compared to previous years. Stripe rust infections in the southern U.S. were less severe and extensive than 2003 and provided less inoculum for the northern wheat growing area.

**Central Plains.** In mid-May, stripe rust was at trace levels on flag leaves in a central Kansas field. In late May, stripe rust was at trace–10 % severity on flag leaves in southeast and south central Kansas fields. Stripe rust was much lighter than last year in this area. In 2003 there was 10.6 % loss to stripe rust in Kansas, whereas in 2004, there was 0.1 % loss (<http://www.cdl.umn.edu/loss/loss.html>).

In late May, low levels of wheat stripe rust were found on flag leaves in north central Kansas (Fig 2). The warm and dry conditions in May reduced further development of stripe rust in Kansas.

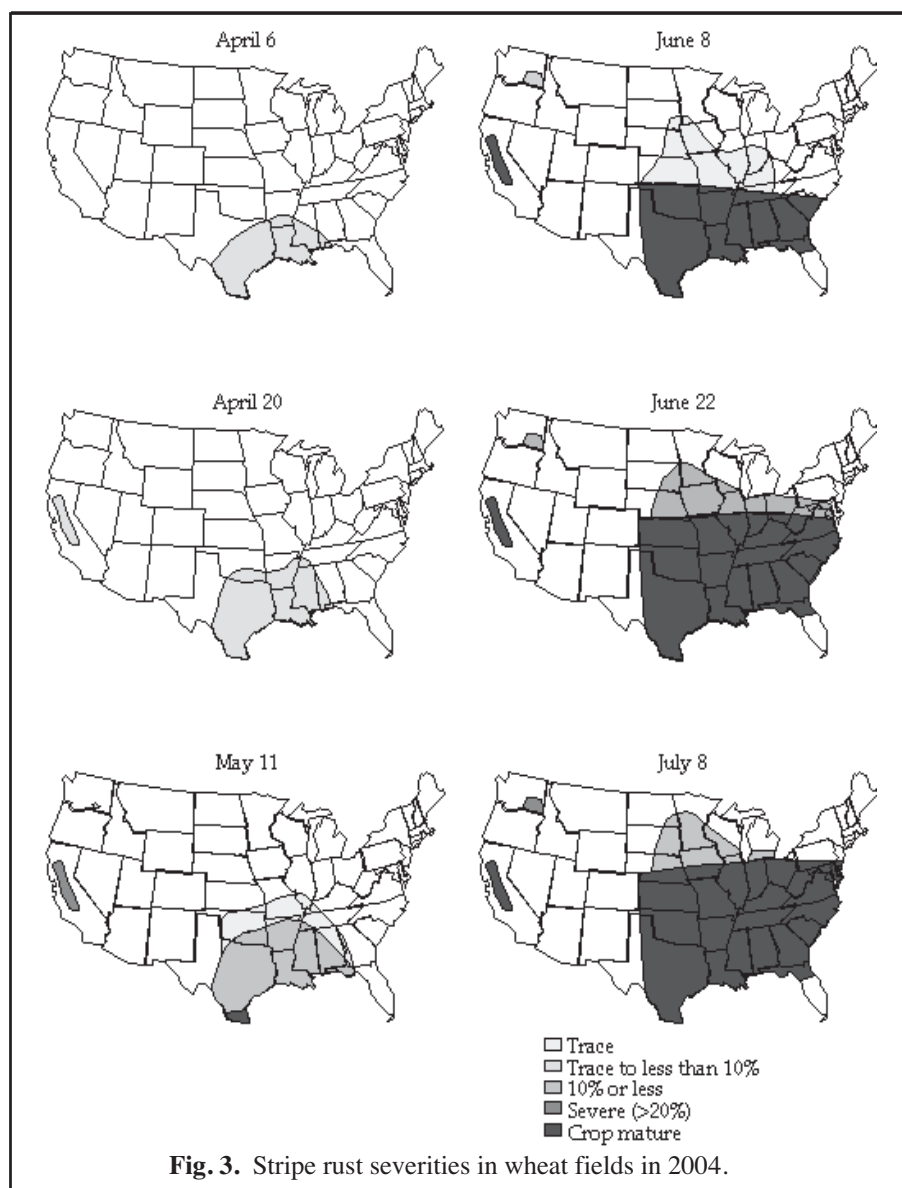
In mid-June, stripe rust was not observed in fields or plots in Nebraska, possibly due to the heavy leaf rust infections.



**Fig. 2.** Agroecological areas for *Puccinia triticina*.

**Table 4.** Estimated losses in winter wheat due to rust in 2004 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to					
				Stem rust		Leaf rust		Stripe rust	
				Percent	1,000 bushels	Percent	1,000 bushels	Percent	1,000 bushels
AL	60	48.0	2,880	0.0	0.0	1.0	29.1	T	T
AR	620	53.0	32,860	0.0	0.0	T	T	2.0	670.6
CA	320	85.0	27,200	0.0	0.0	T	T	5.0	1,431.6
CO	1,700	27.0	45,900	0.0	0.0	T	T	T	T
DE	47	58.0	2,726	0.0	0.0	T	T	0.0	0.0
FL	15	45.0	675	0.0	0.0	1.0	6.8	T	T
GA	190	45.0	8,550	0.0	0.0	1.0	86.4	0.0	0.0
ID	700	90.0	63,000	0.0	0.0	T	T	T	T
IL	900	59.0	53,100	0.0	0.0	1.0	536.4	T	T
IN	440	62.0	27,290	0.0	0.0	1.0	275.6	T	T
IA	24	55.0	1,320	0.0	0.0	T	T	T	T
KS	8,500	37.0	314,500	0.0	0.0	1.4	4,470.1	0.1	319.2
KY	380	54.0	20,520	0.0	0.0	T	T	T	T
LA	165	50.0	8,250	0.0	0.0	1.5	131.6	4.5	394.9
MD	145	59.0	8,555	0.0	0.0	T	T	0.0	0.0
MI	640	64.0	40,960	0.0	0.0	1.0	413.7	T	T
MN	25	40.0	1,000	0.0	0.0	1.0	10.1	T	T
MS	135	53.0	7,155	0.0	0.0	1.0	73.8	2.0	147.5
MO	930	52.0	48,360	0.0	0.0	1.0	488.5	T	T
MT	1,630	41.0	66,830	0.0	0.0	T	T	1.0	675.1
NE	1,650	37.0	61,050	0.0	0.0	3.0	1,888.1	T	T
NJ	24	47.0	1,128	0.0	0.0	T	T	0.0	0.0
NM	300	26.0	7,800	0.0	0.0	0.0	0.0	0.0	0.0
NY	100	53.0	53,300	0.0	0.0	T	T	0.0	0.0
NC	460	50.0	23,000	0.0	0.0	T	T	0.0	0.0
ND	225	44.0	9,900	0.0	0.0	1.0	100.0	T	T
OH	890	62.0	55,180	0.0	0.0	1.0	557.4	T	T
OK	4,700	35.0	164,500	0.0	0.0	1.5	2,517.9	0.5	839.3
OR	780	61.0	47,580	0.0	0.0	0.2	98.3	3.0	1,474.6
PA	135	49.0	6,615	0.0	0.0	T	T	0.0	0.0
SC	180	44.0	7,920	0.0	0.0	0.5	15.9	0.0	0.0
SD	1,250	45.0	56,250	0.0	0.0	1.0	568.2	T	T
TN	280	49.0	13,720	0.0	0.0	T	T	T	T
TX	3,500	31.0	108,500	0.0	0.0	4.7	5,477.4	2.2	2,563.9
UT	120	43.0	5,160	0.0	0.0	0.0	0.0	0.0	0.0
VA	180	55.0	9,900	0.0	0.0	0.1	9.9	0.0	0.0
WA	1,750	67.0	117,250	0.0	0.0	T	T	1.5	1,783.5
WV	5	52.0	260	0.0	0.0	T	T	0.0	0.0
WI	225	69.0	12,600	0.0	0.0	1.0	131.2	T	T
WY	135	26.0	3,510	0.0	0.0	0.0	0.0	0.0	0.0
Total	34,455	43.5	1,498,744		0.0		17,886.4		10,302.2
U.S. % loss				0.00		1.02		0.67	
U.S. Total	34,462	43.5	1,499,434						



**Fig. 3.** Stripe rust severities in wheat fields in 2004.

**Northern Plains.** In early June, stripe rust was found in winter wheat plots in east central South Dakota.

In mid-June, trace levels of stripe rust were in winter wheat fields in south central South Dakota, and in fields of spring and winter wheat in eastern South Dakota (Fig. 3). In winter wheat plots at Brookings, most lines had trace levels of stripe rust infection, however a few plots had very high levels of infection on flag and lower leaves. By the third week in June, trace levels of stripe rust were on spring wheat in St. Paul, Minnesota plots.

In 2003, in early June, traces of stripe rust were found in winter wheat plots in east central Minnesota, but in 2004 stripe rust infections were not found until mid-June at this location.

In early July, stripe rust severity levels of 60 % were present in west central Minnesota spring wheat fields and plots (Fig. 3). The cultivars Trooper and Walworth were the most susceptible with stripe rust infections over 50 %. Most of the commonly grown spring wheats have moderate to high

resistance to stripe rust. The very cool temperatures with sufficient moisture levels were conducive for stripe rust development in the north central region.

In mid-July, hot temperatures arrested development of stripe rust on spring wheat in the northern Great Plains. In late July, a spring wheat field in north central Minnesota had 5 % severity where night time temperatures had been more conducive for rust infection.

**Louisiana, Arkansas, and Missouri.** In late February, low levels of stripe rust infections were in southern and east central Louisiana fields. By early April, rust had increased and these fields were sprayed for rust control. By mid-April in northeast Louisiana, stripe rust was severe in soft red winter wheat varietal plots. Some fields were sprayed to reduce losses due to rust. Significant amounts of stripe rust have occurred in five of the last seven years in Louisiana.

In late March, wheat stripe rust was found in fields throughout southeast Arkansas and fungicide application was recommended. In mid-April in southwest Arkansas wheat plots, little stripe rust was found on the most commonly grown varieties. In late April, stripe rust was at trace levels in eastern and northern Arkansas. By early May, in northern Arkansas, some cultivars had 100 % stripe rust severities. In mid-May, stripe rust development had ceased in Arkansas because the high temperatures at night were not conducive for stripe rust increase.

**Table 5A.** Estimated losses in spring wheat due to rust in 2004 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to					
				Stem rust		Leaf rust		Stripe rust	
				Percent	1,000 bushels	Percent	1,000 bushels	Percent	1,000 bushels
CO	14	70.0	980	0.0	0.0	T	T	T	T
ID	490	79.0	38,710	0.0	0.0	0.2	78.0	0.5	194.9
MN	1,610	55.0	88,550	T	T	10.0	9,838.9	T	T
MT	2,850	31.0	88,350	0.0	0.0	T	T	T	T
NE	6	105.0	630	0.0	0.0	0.0	0.0	0.0	0.0
ND	5,950	41.0	243,950	T	T	3.0	7,544.8	T	T
OR	175	48.0	8,400	0.0	0.0	1.0	89.4	5.0	446.8
SD	1,530	47.0	71,910	0.0	0.0	2.0	1,467.6.5	T	T
UT	12	58.0	696	0.0	0.0	0.0	0.0	0.0	0.0
WA	525	50.0	26,250	0.0	0.0	T	T	3.0	811.9
WI	6	42.0	252	0.0	0.0	T	T	0.0	0.0
WY	6	40.0	240	0.0	0.0	0.0	0.0	0.0	0.0
Total from above									
	13,174	43.2	568,910		T		11,306.5		1,453.6
U.S. % loss				T		1.94		0.24	
U.S. total									
	13,174	43.2	568,910						

**Table 5B.** Estimated losses in durum wheat due to rust in 2004 (T = trace).

State	1,000 acres harvested	Yield in bushels per acre	Production, 1,000 bushels	Losses due to					
				Stem rust		Leaf rust		Stripe rust	
				Percent	1,000 bushels	Percent	1,000 bushels	Percent	1,000 bushels
AZ	100	97.0	9,603	0.0	0.0	0.0	0.0	0.0	0.0
CA	120	90.0	9,000	0.0	0.0	0.0	0.0	5.0	473.7
MN	1	55.0	55	0.0	0.0	0.0	0.0	0.0	0.0
MT	545	33.0	17,985	0.0	0.0	0.0	0.0	0.0	0.0
ND	1,600	33.0	52,800	0.0	0.0	T	T	0.0	0.0
SD	18	25.0	450	0.0	0.0	0.0	0.0	0.0	0.0
Total from above									
	2,363	38.0	89,893		0.0		T		473.7
U.S. % loss				0.00		T		0.52	
U.S. Total									
	2,363	38.0	89,893						

In late May, 5–10 % stripe rust severities were observed in soft red winter wheat fields in west central Missouri. Stripe rust severity was less than last year in this area and the crop was 7–10 days earlier than normal. Traces of stripe rust were observed in plots and fields in northeastern Missouri in early June.

**Midwest.** In early May, stripe rust was light in wheat fields in southwestern Illinois. Traces of stripe rust were in west central Indiana plots in early June.

During the second week in June, stripe rust foci of 10 % severity were located in winter wheat plots and fields in northern Indiana and south central Wisconsin.

During the second week in June, traces of stripe rust were found in plots in central, northeast and northwest Ohio.

In early July, 20 % severities were observed in fields of soft red winter wheat in northeastern Wisconsin.

**California** – Stripe rust on wheat was first detected on 12 February in the UC Regional Wheat Nursery in the Sacramento/San Joaquin Delta nursery in California. Rust was scattered throughout the nursery in light amounts (less than 1 % incidence), but pustules on infected plants were sporulating profusely. Infected leaves had up to 30 % severity. By early March, wheat stripe rust had increased to 50 % severity and 20 % incidence in the nursery at Sacramento/San Joaquin Delta. The crop was in late jointing stage. In early March, low levels of wheat stripe rust were found in nurseries in Madera county and Davis, California.

In Mexico, wheat stripe rust in the southern Sonora state was not as severe as in previous years. However, northern Sonora and the neighboring state of Baja California had more rainfall. This area (Mexicali Valley) is close to a U.S. wheat growing area where stripe rust could have an economic impact.

In mid-April, wheat stripe rust was severe in susceptible varieties in nurseries in the Central Valley and Sacramento Valley of California. In the same area stripe rust was at low to moderate severities on durum varieties. Stripe rust infection foci were observed in fields in the Sacramento Valley.

In mid-July, spring wheat plots had 40 % stripe rust severities spring wheat plots at the early dough growth stage in northeastern California at Tulelake. Stripe rust foci also were detected in plots of wheat at 90 % severity, and 30 % incidence in a north central California nursery.

In California, yield losses from stripe rust were considerably less than in 2003 because of the wide-use of resistant varieties and the late development of heavy rust infections (Table 4, p. 217). One concern in 2004 was that new rust races have developed that are virulent to the resistance that was effective in 2003 and much of the 2004 season. These races may survive in the stripe rust population and appear in higher frequency next season.

**Pacific Northwest.** In early March, severity levels of 30 % were in winter wheat fields and plots in northwestern Washington. Stripe rust was uniformly distributed in commercial fields. Stripe rust severity and distribution patterns were typical for this area. In late March stripe rust was not found on the eastern side of the Rocky Mountains in Washington.

During the last week of April, stripe rust was starting to increase in experimental plots in northeast Oregon and southeast Washington. Near Connell, Washington, severity levels of 20 % were in fields planted with the HRWW Hatton. In 2004, the appearance of stripe rust was much later than 2003, because of the dry weather in the autumn of 2003 that reduced fall infection and a cold winter that reduced winter survival. The stripe rust infections were on the top leaves, indicating infections occurred mostly after the winter season. The rust infected winter wheat produced rust spores that infected spring wheat crops in central and eastern Washington and northern Idaho.

By late May, wheat stripe rust was observed on susceptible spring and winter wheat cultivars growing in fields and plots in central and eastern Washington and northern Idaho.

In late June, wheat stripe rust was developing very rapidly in fields of susceptible winter and spring wheat cultivars in eastern Washington. Many of these cultivars have high temperature adult plant resistance, which reduced rust losses. Some fields had incidence levels of 60 % stripe rust and severity levels of 20%. Fungicides were applied on susceptible wheat fields. Plots of susceptible lines had 80 % severities near Pullman, Washington. In 2004, yield losses to stripe rust occurred in the Pacific Northwest, but were less than 2003 (<http://www.cdl.umn.edu/loss/loss.html>).

**NEBRASKA****UNIVERSITY OF NEBRASKA–LINCOLN AND USDA–ARS, WHEAT, SORGHUM  
& FORAGES UNIT****Lincoln, NE, 68583, USA.**

P.S. Baenziger, D. Baltensperger, L. Nelson, I. Dweikat, A. Mitra, T. Clemente, S. Sato, J. Watkins, J. Schimelfenig, and G. Hein (University of Nebraska); and R.A. Graybosch, L. Divis, R. French, and D. Stenger (USDA–ARS).

***Wheat production.***

The 2004 Nebraska Wheat Crop was estimated at 61,100,000 bu, which represented a 37 bu/acre state average yield on 1,650,000 harvested acres. 1,850,000 acres were planted to winter wheat in the autumn of 2003. The 2004 crop was 27 % lower than the 2003 crop (79,900,000 bu, which represented a 47 bu/acre state average yield on 1,700,000 harvested acres).

***New cultivars.***

P.S. Baenziger, D. Baltensperger, L. Nelson, J. Watkins, J. Schimelfenig, G. Hein, and R. Graybosch.

In 2004, two new cultivars (**Hallam** and **Infinity**) were recommended for release. Infinity CL is a HRWW cultivar developed coöperatively by the Nebraska Agricultural Experiment Station and the USDA–ARS and released in 2005 by the developing institutions. Infinity CL contains a patented gene owned by BASF and who retains ownership of the gene. Infinity CL was released primarily for its superior adaptation to rainfed-wheat production systems in Nebraska and counties in adjacent states. The name Infinity CL was chosen because it is a Clearfield™ wheat that will be used with Beyond® herbicide. Infinity CL was selected from the cross ‘Windstar//Millennium sib/Above sib’. Infinity CL was evaluated as NH01046 in Nebraska yield nurseries starting in 2002, and in Nebraska and Wyoming cultivar performance trials in 2003 to 2004. In the Nebraska cultivar performance trials, Infinity CL has performed well throughout most of Nebraska. The average Nebraska rainfed yield of Infinity CL of 3,870 kg/ha (27 environments from 2003–04) was lower than the yield of Wesley (3,990 kg/ha), similar to that of Millennium (3,860 kg/ha), and higher than those of Wahoo (3,790 kg/ha) and Alliance (3,620 kg/ha). The average Wyoming rainfed yield of Infinity CL of 2,220 kg/ha (five environments from 2003–04) was lower than that of Goodstreak (2,350 kg/ha), similar to that of Buckskin (2,280 kg/ha), and higher than that of Above (2,080 kg/ha). Infinity CL has acceptable performance under irrigation, but other wheat cultivars with superior performance, especially with better straw strength (described below), would be recommended.

Hallam is a HRWW cultivar developed coöperatively by the Nebraska Agricultural Experiment Station and the USDA–ARS and released in 2005 by the developing institutions. Hallam was released primarily for its superior adaptation to rainfed wheat production systems in eastern Nebraska. The name Hallam was chosen to honor Hallam, NE, a town and its people rebuilding after a tornado. Hallam was selected from the cross ‘Brule/Bennett//Niobrara’ that was made in 1992. Hallam was evaluated as NE98471 in Nebraska yield nurseries starting in 1999, in the Northern Regional Performance Nursery in 2001 and 2002, and in Nebraska cultivar performance trials in 2002 to 2004. In the Nebraska cultivar performance trials, Hallam appears to be narrowly adapted and performs best in eastern Nebraska. The average Nebraska rainfed yield of Hallam of 4,110 kg/ha (41 environments from 2002 to 2004) was greater than the yields of Wahoo (4,030 kg/ha), Alliance (3,880 kg/ha), and Harry (4,000 kg/ha), but was lower than those of Millennium (4,180 kg/ha), and Wesley (4,210 kg/ha). In its primary area of adaptation (eastern NE), Hallam (five environments) has yielded 4,540 kg/ha, which was greater than those of Wesley (4,150 kg/ha), Millennium (4,250 kg/ha), Wahoo (3,940 kg/ha), and Alliance (3,900 kg/ha). Hallam was tested in the Northern Regional Performance Nursery in 2001 and 2002 and ranked 14th out of 30 in 2001 (12 environments) and 4th of 25 entries in 2002 (13 environments) and averaged 100 kg/ha more grain yield than Nekota.

---

***Increase of new experimental lines.***

P.S. Baenziger.

Based on last year's results and our recent releases, we have decided to increase one line, **NE99495**. NE99495 is a HRWW with the pedigree 'Alliance/Karl 92'. The cross was made in 1993. NE99495 is an F<sub>3</sub>-derived line that was selected in the F<sub>4</sub> generation. The F<sub>1</sub> generation was grown in the greenhouse in 1993–94. The F<sub>2</sub> and F<sub>3</sub> generations were grown in bulk at the Agricultural Research and Development Center at Ithaca, NE, in 1995 and 1996, respectively. Random heads were chosen from the F<sub>3</sub> bulk and planted as head rows, which were harvested in 1997. The F<sub>3</sub>-derived F<sub>5</sub> family was harvested as a single observation plot in 1998. NE99495 was identified in 1999 and was grown at six unreplicated locations in 1997. NE99495 has been tested in replicated trials at six to seven locations/year from 2000 to present. In addition, NE99495 was tested in the Northern Regional Performance Nursery in 2002 and 2003 and in Nebraska cultivar performance trials in 2003 and 2004. NE99495 is semidwarf wheat with medium plant height for a semidwarf cultivar and acceptable winter hardiness for production in Nebraska. NE99495 is slightly later than Alliance and slightly earlier than Millennium for flowering date.

***Hard white wheat development.***

R.A. Graybosch, P.S. Baenziger, B. Beecher, D. Baltensperger, and L. Nelson.

The following hard white wheats are entered in the 2005 Nebraska Statewide Small Grains Variety trial for testing and possible release: NW99L7068, NW97S139-1, NW98S097, and NP-02. NW98S097 consistently has demonstrated low levels of grain PPO. We anticipate at least one of these lines will be approved for cultivar release.

***Wheat quality research.***

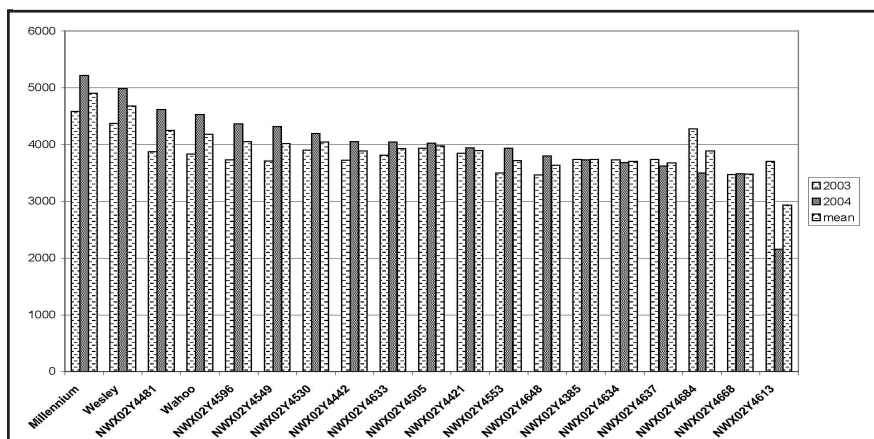
R.A. Graybosch, P.S. Baenziger, and M. Shipman.

To determine whether or not increased expression of glutenin genes in wheat endosperm can result in improved baking quality of hard winter wheat, we have developed winter wheats carrying transgenes that independently elevate expression of the HMW glutenin subunits 5 and 10. Five genetic populations, each composed of a series of transgenic and non-transgenic sister lines, were seeded in an augmented design, along with strong gluten check cultivars, in the autumn of 2003. The study contained approximately 60 transgenic lines and an equal number of nontransgenic sister lines. From each line, 12 head selections were obtained and tested for continued expression of the transgenic glutenins. A selected group of stably expressing lines was reseeded, along with controls and nonexpressing sister lines. Quality work on year one materials has revealed that total grain protein content was not affected, but mixograph mixing properties were drastically altered, demonstrating that processing quality, even in strong gluten backgrounds, can be altered by over-expressing specific endosperm proteins.

***Winter waxy wheat breeding.***

R.A. Graybosch and P.S. Baenziger.

Approximately 30 winter waxy wheats were advanced to either their second or third year of yield testing in Nebraska. In addition, 80 new winter waxy wheats were selected at Yuma, AZ, and advanced to a two location preliminary yield trial in Nebraska. After several cycles of mating and selection, waxy winter wheats now have been developed with grain yields nearly equal to those of current cultivars (Fig. 1, p. 223). A bit of a yield drag remains, but we anticipate that the gap between waxy and wild-type wheats shortly will be erased by continued breeding efforts.



**Fig. 1.** Mean grain yield (kg/ha) of experimental waxy wheats and check cultivars from four Nebraska environments. NWX prefix designates a fully waxy line. Millennium, Wesley, and Wahoo are current cultivars.

## Personnel.

Dr. M Liakat Ali joined the project as a postdoctoral scientist who will be studying recombinant inbred chromosome lines for chromosome 3A. Dr. Brian Beecher accepted a position with USDA-ARS at Pullman, WA.

## Publications.

Baenziger PS, Erayman M, Budak H, and Campbell TB. 2004. Breeding pure line cultivars. **In:** Encyclopedia of Plant and Crop Science, 1st Ed (Goodman RM Ed). Marcel Dekker, Inc. New York, NY.

Pp.196-201.

- Baenziger PS, McMaster GS, Wilhelm WW, Weiss A, and Hays CJ. 2004. Putting genes into genetic coefficients. *Field Crop Res* 90:133-143.
- Baenziger PS, Beecher B, Graybosch RA, Baltensperger DD, Nelson LA, Krall JM, McVey DV, Watkins JE, Hatchett JH, and Chen MS. 2004. Registration of 'Goodstreak' wheat. *Crop Sci* 44:1473-1474.
- Baenziger PS, Beecher B, Graybosch RA, Baltensperger DD, Nelson LA, Krall JM, McVey DV, Watkins JE, Hatchett JH, and Chen MS. 2004. Registration of 'Harry' wheat. *Crop Sci* 44:1474-1475.
- Budak H, Baenziger PS, Beecher B, Graybosch RA, Campbell BT, Shipman M, Erayman M, and Eskridge KM. 2004. The effect of introgressions of wheat D-genome chromosomes into 'Presto' triticale. *Euphytica* 137:261-270.
- Campbell BT, Baenziger PS, Eskridge KM, Budak H, Streck NA, Weiss A, Gill KS, and Erayman M. 2004. Using environmental covariates to explain genotype x environments and QTL x environment interactions for agronomic traits on chromosome 3A of wheat. *Crop Sci* 44:620-627.
- Erayman M, Sandhu D, Sidhu D, Dilbirligi M, Baenziger PS, and Gill KS. 2004. Demarcating the gene-rich regions of the wheat genome. *Nucl Acids Res* 32:3546-3565.
- Graybosch RA. 2004. Grain Crops: Overview. **In:** Encyclopedia of Grain Science. Vol 2 (Wrigley C, Corke H, and Walker CE, Eds). Elsevier Ltd., Oxford, UK. Pp. 46-55.
- Graybosch RA. 2004. Potential for gene flow from cultivated wheat to weedy relatives in the Great Plains of North America. **In:** Biological Resources and Migration (Werner D Ed). Springer Verlag, Berlin. Pp. 27-34.
- Graybosch RA, Ames N, Baenziger PS, and Peterson CJ. 2004. Genotypic and environmental modification of Asian noodle quality of hard winter wheat. *Cereal Chem* 81:19-25.
- Graybosch RA, Peterson CJ, and Chung OK. 2004. Registration of N95L11881 and 97L9521 strong gluten 1BL·1RS wheat germplasm lines. *Crop Sci* 44:1490-1491.
- Graybosch RA, Peterson CJ, Porter DR, and Chung OK. 2004. Registration of N96L9970 greenbug resistant wheat. *Crop Sci* 44:1492-1493.
- Graybosch RA, Souza EJ, Berzonsky WA, Baenziger PS, McVey DV, and Chung OK. 2004. Registration of nineteen waxy spring wheats. *Crop Sci* 44:1491-1492.
- Haliloglu K and Baenziger PS. 2003. The effects of age and size of wheat (*Triticum aestivum* L.) anther culture-derived embryos on regeneration of green and albino plantlets. *Israeli J Plant Sci* 51:207-212.
- Kim K-M, Lee DE, Song H, Kuk YI, Guh JO, Baenziger PS, and Back K. 2004. Influence of a selectable marker gene hpt on agronomic performance in transgenic rice. *Cereal Res Commun* 32:9-16.
- Kim W, Johnson JW, Baenziger PS, Lukaszewski AJ, and Gaines CS. 2004. Agronomic effect of wheat-rye translocation carrying rye chromatin (1R) from different sources. *Crop Sci* 44:1254-1258.
- Kuleung C, Baenziger PS, and Dweikat I. 2004. Transferability of SSR markers among wheat, rye, and triticale. *Theor Appl Genet* 108:1147-1150.
- Mahmood A, Baenziger PS, Budak H, Gill KS, and Dweikat I. 2004. The use of microsatellite markers for the detection of genetic similarity among winter bread wheat lines for chromosome 3A. *Theor Appl Genet* 109:1494-1503.

- Mater Y, Baenziger PS, Gill KS, Graybosch RA, Whitcher L, Baker C, Specht J, and Dweikat I. 2004. Linkage mapping of powdery mildew and greenbug resistance genes on recombinant 1RS from 'Amigo' and 'Kavkaz' wheat-rye translocations of chromosome 1RS·1AS. *Genome* 47:292-298.
- Xue Q, Weiss A, Arkebauer TJ, and Baenziger PS. 2004. Influence of soil water status and atmospheric vapor pressure deficit on leaf gas exchange in field-grown winter wheat. *Env Exp Bot* 51:93-181.
- Xue Q, Weiss A, and Baenziger PS. 2004. Predicting phenological development in winter wheat. *Climate Res* 25:243-252.
- Xue Q, Weiss A, and Baenziger PS. 2004. Predicting leaf appearance in field-grown winter wheat: evaluating linear and non-linear models. *Ecol Modeling* 175:261-270.

## **NORTH DAKOTA**

### **USDA–ARS CEREAL CROPS RESEARCH UNIT Northern Crop Science Laboratory, Fargo, ND, USA.**

#### ***A hard red spring wheat intervarietal genetic linkage map constructed using microsatellite and target region amplification polymorphism (TRAP) markers.***

Zhaohui Liu, James A. Anderson, Jinguo Hu, Timothy L. Friesen, Jack B. Rasmussen, and Justin D. Faris.

Efficient user-friendly methods for mapping plant genomes are highly desirable for the identification of QTL, genotypic profiling, genomic studies, and MAS. SSR (microsatellite) markers are user-friendly and efficient in detecting polymorphism, but they detect few loci. Target region amplification polymorphism (TRAP) is a relatively new PCR-based technique that detects a large number of loci from a single reaction without extensive pre-PCR processing of samples. In this work, we used both SSRs and TRAPs to generate over 700 markers for the construction of a genetic linkage map in a hard red spring wheat intervarietal recombinant inbred population. A framework map consisting of 352 markers accounted for 3,045 cM with an average density of one marker per 8.7 cM. On average, SSRs detected 1.9 polymorphic loci per reaction, whereas TRAPs detected 24. Both marker systems were suitable for assigning linkage groups to chromosomes using wheat aneuploid stocks. We demonstrated the utility of the maps by identifying major QTL for days to heading and reduced plant height on chromosomes 5A and 4B, respectively. This work indicates that TRAPs are highly efficient for genetic mapping in wheat. The maps developed will be useful for the identification of quality and disease resistance QTL that segregate in this population.

#### ***Mapping of toxin sensitivity and QTL analysis of seedling resistance to *Stagonospora nodorum* blotch in an intervarietal hard red spring wheat population.***

Zhaohui Liu, Timothy L. Friesen, Steven W. Meinhardt, Jack B. Rasmussen, and Justin D. Faris.

*Stagonospora nodorum* blotch (SNB) is an economically important foliar and glume disease in the major wheat growing areas of the world. We previously identified a host-selective toxin (SnTox1) produced by the isolate Sn2000 of *S. nodorum* and mapped the gene (*Snn1*) conditioning sensitivity to chromosome 1BS in the International Triticeae Mapping Initiative (ITMI) population. Here, we evaluated SnTox1 sensitivity and resistance to SNB caused by Sn2000 in a population of RILs derived from a cross between Grandin and BR34. In this population, sensitivity to partially purified SnTox1 mapped to the long arm of chromosome 5B and cosegregated with *Tsn1*, which confers sensitivity to Ptr ToxA produced by the tan spot fungus *P. tritici-repentis*. The *tsn1* locus underlied a major QTL for resistance to SNB and explained 62 % of the phenotypic variation indicating that SnTox1 plays an important role in causing disease. Additional minor QTL were detected on 5BL and 1BS. These results suggest that SnTox1 can recognize multiple host genes to cause necrosis, and that the product of *Tsn1* can serve as a target for proteinaceous toxins produced by different pathogenic fungi.

***Identification of quantitative trait loci for race-nonspecific resistance to tan spot in wheat.***

Justin D. Faris and Timothy L. Friesen.

Tan spot, caused by *P. tritici-repentis* (Ptr), is an economically important foliar disease in the major wheat-growing areas throughout the world. Multiple races of the pathogen have been characterized based on their ability to cause necrosis and/or chlorosis on differential wheat lines. In this research, we evaluated a population of RILs derived from a cross between the common wheat cultivars Grandin and BR34 for reaction to tan spot caused by Ptr races 1, 2, 3, and 5. Composite interval mapping revealed QTL on the short arm of chromosome 1B and the long arm of chromosome 3B significantly associated with resistance to all four races. The effects of the two QTL varied for the different races with the 1B QTL explaining from 13 to 29 percent of the phenotypic variation, whereas the 3B QTL explained from 13 to 41 percent of the variation. With the exception of a minor QTL on the short arm of chromosome 3B associated with resistance to race 3, no other significant QTL were detected. The host-selective toxin Ptr ToxA, which is produced by races 1 and 2, was not a significant factor in the development of disease in this population. The race-nonspecific resistance mechanisms derived from BR34 may preclude the recognition of the gene-for-gene interaction known to be associated with the wheat-tan spot system.

***Comparative analyses of a gene rich region of wheat chromosome 5B with rice using expressed sequences.***

Huangjun Lu and Justin D. Faris.

EST and genome-sequencing data have provided the basis for comparative genomics between wheat and rice. In this study, markers representing expressed sequences within the wheat deletion interval 5BL 0.75–0.76 were used to determine the level of colinearity of this genomic region with rice. A population consisting of 117 recombinant substitution lines (RSLs) derived from the cross ‘Chinese Spring (CS)/CS *T. turgidum* subsp. *dicoccoides* chromosome 5B substitution line (CS-Dic5B)’ was used to develop a genetic map corresponding to the deletion interval. We mapped 35 expressed sequence markers as RFLPs or SSCPs, which resulted in a map of 51.4 cM in length. Of these markers, 19 (54 %) detected homologous sequences in rice genome. Analyses of colinearity using expressed sequences that detected rice homologs indicated a lack of conservation. Small regions of colinearity with rice chromosomes 3 and 9 were found, but multiple breaks, interruptions, and rearrangements exist. These anomalies will make it extremely difficult to use rice as a model for positional cloning of wheat genes in this region due to the lack of conservation.

***Towards positional cloning of the *Tsn1* gene in wheat.***

Huangjun Lu, John P. Fellers, Timothy L. Friesen, Steven W. Meinhardt, Karri M. Haen, and Justin D. Faris.

*Tsn1* conditions sensitivity to a host-selective proteinaceous toxin (Ptr ToxA) produced by the pathogenic fungus *P. tritici-repentis*. A large  $F_2$  population consisting of 5,378 gametes was produced to develop a high-resolution map for positional cloning of the gene. Chromosome walking in conjunction with complete sequencing of BACs identified in the Langdon durum BAC library was initiated from two AFLP-derived markers *Xfcg17* and *Xfcg9* that flank the *Tsn1* gene at 0.24 and 0.46 cM, respectively. So far, three BACs on the *Xfcg17* side of the gene have been sequenced. The new markers that were developed from these BACs spanning 215 kb cosegregated in the  $F_2$  population, suggesting that recombination is greatly suppressed in the vicinity of *Xfcg17*. On the *Xfcg9* side of the gene, a contig of more than 550 kb has been constructed, and we have identified a candidate gene on the end of the contig that cosegregates with *Tsn1*. Physical to genetic distance ratios in the *Tsn1* region ranged from 230 kb/cM to 10 Mb/cM. From the regions that have been sequenced, we have identified about 25 genes, many of which are genes that encode cell wall-associated receptors or kinases and DHHC type zinc finger proteins. The cloning and characterization of *Tsn1* will increase our knowledge of the host-pathogen interaction.

---

***Isolation and characterization of the major domestication gene *Q* in wheat.***

Kristin J. Simons, John P. Fellers, Harold N. Trick, Zengcui Zhang, Bikram S. Gill, and Justin D. Faris.

The *Q* gene is largely responsible for the domestication of wheat because it confers the square spike phenotype and the free-threshing character. *Q* also pleiotropically influences many other domestication-related traits such as glume shape and tenacity, rachis fragility, spike length, plant height, and ear emergence time. We isolated the *Q* gene and verified its identity by analysis of knockout mutants and transformation. We found that *Q* is a floral homeotic gene with similarity to the AP2 class of transcription factors. Ectopic expression analysis allowed us to observe both silencing and overexpression effects of *Q*. Variation in spike compactness and plant height was directly correlated with the degree of ectopic expression, which verified previous results regarding the dosage effects of *Q*. Other characters such as rachis fragility, glume shape, and glume tenacity, mimicked the *q* phenotype in transgenic plants exhibiting silencing of the transgene and the endogenous *Q* gene. Sequence analysis of the gene in multiple free-threshing and non free-threshing genotypes suggests that *Q* arose from *q* through mutation.

***Saturation mapping of the FHB resistance QTL *Qfhs.ndsu-3A* in tetraploid wheat.***

Xunfen Chen, Jinguo Hu, Shahryar Kianian, Xiwen Cai, and Justin D. Faris.

The major FHB resistance QTL *Qfhs.ndsu-3AS* was identified from a wild tetraploid wheat accession *T. turgidum* subsp. *dicoccoides* and mapped within a 29.3 cM interval on chromosome 3A. A mapping population of 83 recombinant inbred chromosome lines (RICLs) derived from a cross between the *T. turgidum* subsp. *durum* cultivar Langdon (LDN)-*T. turgidum* subsp. *dicoccoides* substitution line 3A and LDN has been used for saturation mapping of this QTL region in the present study. To date, we have assigned 30 new molecular markers to the QTL region and located the QTL within a 10.1 cM chromosomal interval, which is about three times smaller than the previous interval (29.3 cM). Comparative mapping suggested that the FHB resistance QTL *Qfhs.ndsu-3AS* and *Qfhs.ndsu-3BS* localized on the short arm of chromosome 3A and 3B, respectively, are not homeoloci.

***Identification of a Fusarium head blight resistance QTL on chromosome 6B in tetraploid wheat.***

Robert W. Stack and Justin D. Faris.

Fusarium head blight is one of the most devastating diseases of bread and durum wheat. Resistant sources of hexaploid bread wheat have been identified and are currently being employed in breeding programs, but development of resistant tetraploid durum wheat has met with less success. Resistance has been identified in *T. turgidum* subsp. *dicoccoides*, a wild tetraploid relative, which readily hybridizes with durum wheat. Evaluation of Langdon durum-*T. turgidum* subsp. *dicoccoides* (LDN-DIC) disomic chromosome substitution lines indicated that *T. turgidum* subsp. *dicoccoides* chromosome 6B contributed a significant level of resistance. In this work, we evaluated a population of 85 recombinant inbred chromosome lines (RICLs) derived from LDN x LDN-DIC 6B for reaction to FHB, and surveyed markers along the previously constructed chromosome 6B genetic linkage map for associations with FHB resistance. Simple linear regression and composite interval regression analysis indicated the presence of a QTL on the short arm of 6B. This QTL accounted for about 20 percent of the phenotypic variation for resistance to FHB. It will be beneficial to combine this QTL with others to increase the levels of FHB resistance in durum cultivars.

***Utilization of molecular markers in the characterization and development of germ plasm and genetic stocks in wheat.***

Steven S. Xu, Justin D. Faris, Daryl Klindworth, Xiwen Cai, and Jinguo Hu

Modern molecular marker technologies greatly facilitate the characterization and development of new germ plasm and genetic stocks in crops. During the last 30 years, Dr. L. R. Joppa developed a number of useful germ plasm and genetic stocks in durum and common wheat, including various durum disomic substitutions, translocations, and synthetic hexaploid wheat lines. To provide an efficient means of maintaining these lines, we are extensively characterizing them

using DNA markers and gel electrophoresis of seed storage proteins (glutenin subunits and gliadins). Thus far, three sets of Langdon durum-*T. turgidum* subsp. *dicoccoides* disomic substitution lines, five durum 1D/1A translocation lines, and 40 synthetic wheat lines have been characterized using TRAP (target region amplification polymorphism) and SSR (simple sequence repeat) markers and seed storage proteins. This research resulted in development of about 800 chromosome-specific TRAP markers, identification of unique alleles for glutenin subunits and gliadins, and mapping of introgressed chromosome segments. The developed TRAP markers are currently being used for wheat genome mapping, chromosome identification, and genetic diversity studies. The glutenin subunits from chromosomes 1A, 1B, and 1D, and gliadins for 6A, 6B, and 6D, have been successfully used in the development of a new set of durum D-genome, chromosome substitution lines and for transferring good bread-making quality from bread wheat to durum wheat cultivars. SSR markers closely flanking *Tsn1*, which confers sensitivity to a host selective toxin produced by the tan spot fungus, are being used to eliminate the sensitivity locus from commercial cultivars of bread wheat.

### ***Evaluation of tetraploid wheat germ plasm for resistance to Fusarium head blight.***

R.E. Oliver, S.S. Xu, X. Cai, and R.W. Stack.

Sources of resistance to FHB have been identified and utilized in breeding for FHB resistance in common wheat. However, sources of effective FHB resistance are limited in durum wheat. Attempts to transfer resistance from hexaploid wheat to durum wheat have met with minimal success. In order to identify novel sources of FHB resistance usable for enhancing resistance of durum wheat to FHB, we systematically evaluated 185 accessions of five subspecies under *T. turgidum* for resistance to spread of FHB infection (type-II resistance) in controlled greenhouse condition. These subspecies include Persian wheat (*T. turgidum* subsp. *carthlicum*), cultivated emmer wheat (*T. turgidum* subsp. *dicoccum*), Polish wheat (*T. turgidum* subsp. *polonicum*), oriental wheat (*T. turgidum* subsp. *turanicum*), and poulard wheat (*T. turgidum* subsp. *turgidum*). Preliminary results from this study indicated that four accessions of cultivated emmer wheat and six accessions of Persian wheat had a similar level of resistance as Alsen, a Sumai 3-derived HRSW cultivar in North Dakota. Further evaluations are being conducted to confirm FHB resistance of these cultivated tetraploid wheat accessions in the greenhouse and field. These accessions could serve as novel sources of resistance to develop durum wheat cultivars resistant to FHB.

### **Publications**

- Cai X, Chen PD, Xu SS, Oliver RE, and Chen X. 2005. Utilization of alien genes to enhance Fusarium head blight resistance in wheat. *Euphytica* 140 (In press).
- Faris JD, Friebe B, and Gill BS. 2004. Genome Mapping. **In:** Encyclopedia of Grain Science (Wrigley C Ed). Elsevier, San Diego, CA. Pp. 7-16.
- Friesen TL and Faris JD. 2004. Molecular mapping of resistance to *Pyrenophora tritici-repentis* race 5 and sensitivity to PtrToxB in wheat. *Theor Appl Genet* 109:464-471.
- Haen KM, Lu HJ, Freisen TL, and Faris JD. 2004. Genomic targeting and high-resolution mapping of the *Tsn1* gene in wheat. *Crop Sci* 44:951-962.
- Klindworth DL, Hareland GA, Elias EM, and Xu SS. 2005. Agronomic and quality characteristics of 1AS.1AL-1DL translocation lines of durum wheat carrying *Glu-D1d*. *Crop Sci* 45:77-84.
- Liu ZH, Friesen TL, Meinhardt SW, Ali S, Rasmussen JB, and Faris JD. 2004. QTL analysis and mapping of seedling resistance to *Stagonospora nodorum* leaf blotch in wheat. *Phytopathology* 94:1061-1067.
- Liu ZH, Faris JD, Meinhardt SW, Ali S, Rasmussen JB, and Friesen TL. 2004. Genetic and physical mapping of a gene conditioning sensitivity in wheat to a partially purified host-selective toxin produced by *Stagonospora nodorum*. *Phytopathology*. 94:1056-1060.
- Oliver RE, Cai X, Xu SS, Chen X, and Stack RW. 2005. Wheat-alien species derivatives: a potential source of novel resistance to Fusarium head blight in wheat. *Crop Sci* 45 (In press).
- Xu SS, Friesen TL, and Mujeeb-Kazi A. 2004. Seedling resistance to tan spot and *Stagonospora nodorum* blotch in synthetic hexaploid wheats. *Crop Sci* 44:2238-2245.
- Xu SS, Friesen TL, and Cai X. 2004. Source and genetic control of resistance to *Stagonospora nodorum* blotch in wheat. *Recent Res. Devel Genet Breed* 1:449-469.
- Xu SS, Khan K, Klindworth DL, Faris JD, and Nygard G. 2004. Chromosomal locations of genes for novel glutenin subunits and gliadins in wild emmer wheat (*Triticum turgidum* L. var. *dicoccoides*). *Theor Appl Genet* 108:1221-1228.

---

**OKLAHOMA****OKLAHOMA STATE UNIVERSITY****Department of Plant and Soil Sciences, 368 Ag Hall, Stillwater, OK 74078-6028, USA.**

J.T. Edwards, B.F. Carver, and A.R. Klatt.

***Wheat production and management research.***

Jeff T. Edwards.

Wheat management research at Oklahoma State University continues to focus on the dual-purpose wheat production system (wheat that is both grazed and harvested for grain), which occupies the majority of seeded acreage in Oklahoma. This effort is balanced among three major objectives. The first of these objectives is to identify the physiological parameters that have the greatest impact of fall forage production and recovery from grazing. Factors currently being evaluated include leaf expansion rate, cardinal temperatures, and radiation use efficiency. We plan to use these data to develop a mechanistic understanding of wheat forage production and to establish critical traits to be selected for when breeding for a dual-purpose wheat-production system.

Our second objective is compare management strategies aimed at increasing fall forage production. To meet this objective we are comparing the economic returns of increasing fall wheat forage through variety selection, seeding rate, planting date, or nitrogen rate. From these data we plan to improve our research-driven recommendations to farmers.

Finally, we are coordinating validation/demonstration efforts for sensor-based nitrogen recommendations developed by researchers at Oklahoma State University. Through this work we plan to provide data necessary to fine tune the nitrogen-recommendation algorithm and increase adoption of sensor-based technologies throughout the southern Great Plains.

***Cultivar development and breeding research.***

Brett F. Carver.

The Oklahoma Agricultural Experiment Station and USDA-ARS will jointly announce in May 2005 the release of **Okfield** HRW wheat and **Guymon** HW wheat. Okfield is a Clearfield™ wheat with the pedigree 'TXGH12588-120\*4/FS4//2174'. The germ plasm indicated by FS4 originated with BASF Corporation (formerly American Cyanamid) and provides tolerance to the imidazolinone class of herbicides. Okfield is a more widely adapted cultivar than current Clearfield cultivars, with exception of areas challenged by WSBMV. Okfield shows exceptional recovery from early-planted grazing systems common in the southern Great Plains. Forage accumulation in the early autumn is average, whereas forage regrowth during the grazing period and recovery from grazing are above-average. We do not recommend extremely early seeding of OK02909C, because of its heat-sensitive germination response. Additional attributes compared with Above or AP502CL are slightly better tolerance to leaf rust, as evidenced by extended green-leaf retention and later first-hollow-stem stage (i.e., greater dormancy retention) by several days. Okfield also carries the potential to move into more drought-prone environments in the panhandle where 2174 has experienced some difficulty. Milling and baking characteristics are satisfactory, with above-average kernel size, below-average test weight, intermediate dough strength, and mean wheat protein content of 12.8 %.

One of the hurdles to expansion of the hard white wheat acreage in Oklahoma has been the lack of genetic diversity from which producers can choose to satisfy their specific management needs. Further growth of the HWW industry requires aggressive infusion of new cultivars to motivate producers to adopt HWW cultivars as an addition to, or even a displacement of, the HRW cultivars they currently grow. Guymon marks a new generation of HWW cultivars expected to emerge from the OSU Wheat Improvement Program. Guymon resulted from the cross, Intrada/Platte, and

exceeds the grain yield of Intrada by up to 20 % at similar test weight. Guymon is positioned strictly for the southern High Plains and the panhandle of Oklahoma. Juvenile plant characteristics are befitting for a dual-purpose management system. Autumn forage accumulation up to cattle turnout should approximate, but likely not exceed, that of Intrada; forage regrowth will provide ample winter grazing without breaching winter dormancy. Guymon delivers a relatively high level of wheat protein, which exceeds 14.5 % in the targeted area. Desirable features of bread baking performance, including water absorption and loaf volume, justify its adoption in commercial, large-scale baking operations, but preliminary evaluation of alkaline noodle performance indicates color stability between Intrada (poor) and Platte (good).

A critical feature of this breeding program is what we have coined the **GRAZENGRAIN** breeding system, instituted in 1997, which now generates all breeder lines for replicated yield trials. This breeding system interweaves two components throughout the 10-year cultivar development cycle: 1) multi-environment selection procedures common to any wheat-breeding program and 2) management system-targeted selection both within and between breeding populations. The result is a collection of breeding lines with potentially broader adaptation than selection in the absence of a management system component. This breadth of adaptation is what wheat producers need in the southern Great Plains if they continue to use cultivars indiscriminately in grain-only and early-planted forage-based production systems. Specific components of dual-purpose adaptation that are targeted include: temperature-insensitive germination, coleoptile elongation, early vigor, semierect to semi-prostrate growth habit, rapid leaf expansion, winter dormancy retention, and timely first-hollow-stem development, autumn and winter tillering capacity, and rapid recovery after grazing.

From a broader perspective, selection decisions involve six trait complexes: 1) adaptation (traits governing fitness and yield), 2) disease resistance, 3) insect resistance, 4) stress tolerance, 5) grain quality (physical attributes), and 6) functionality. Specific traits are identified for each complex on our website, [www.wit.okstate.edu](http://www.wit.okstate.edu), and will not be expanded here. We focus selection on durable forms of leaf and stripe rust, including the minor genes of resistance currently being introgressed by A.R. Klatt, as well as BYD tolerance, resistance to the WSBMV/WSSMV complex, and for only the second consecutive year, resistance to powdery mildew. We also intend to continue emphasis on stay-green expression, which provide a comprehensive index for foliar disease tolerance. The traditional suite of quality targets center on test weight, kernel size, protein content, absorption, and dough strength; however, with the emergence in 2005 of the first advanced line trial with strictly hard white wheat, selection efforts will be redirected toward dual-purpose bread and noodle quality.

### ***Variability enhancement/germ plasm development.***

Arthur R. Klatt.

Adapted winter wheat cultivars with stable, long-term leaf rust resistance have not been identified for the southern and central Great Plains. A new cultivar typically maintains leaf rust resistance for a short period of time (2–4 years). In recent years, stripe or yellow rust also has caused significant production losses, and advanced lines in many programs lack good resistance. As a result, a primary objective of the germ plasm-development program at Oklahoma State University is to transfer minor gene resistance for leaf rust and stripe rust from CIMMYT spring wheat germ plasm into adapted winter wheat cultivars. This resistance is characterized by low levels of infection and is based on several minor genes (normally 3–5). Additionally, an extensive crossing program to the synthetic and synthetic wheat derivatives developed by CIMMYT is underway. This effort has multiple objectives, including potentially new genes for leaf and yellow rust resistance, improved kernel size, enhanced stay-green characteristics, drought and heat tolerance, and improved biomass and yield potential. The most advanced materials from this program will be evaluated as F<sub>5</sub>s in the current crop cycle.

Recent research results with irrigated spring wheat indicate that spectral reflectance at selected wavelengths may serve as an effective indirect selection tool for grain yield and biomass production. Research is underway in Oklahoma to verify this relationship in winter wheat. For information regarding this program, contact Dr. Art Klatt, Department of Plant and Soil Sciences, 274 Ag Hall, Stillwater, OK 74078 or via EMAIL at [aklatt@mail.pss.okstate.edu](mailto:aklatt@mail.pss.okstate.edu).

---

**SOUTH DAKOTA****SOUTH DAKOTA STATE UNIVERSITY AND THE USDA-ARS NORTHERN  
GRAIN INSECT RESEARCH LABORATORY (NGIRL).****Plant Science Department, Brookings, SD 57007 U.S.A.**

A.M.H. Ibrahim, S.A. Kalsbeck, R.S. Little, S. Malla, Howard J. Woodard, Anthony Bly, Ron Gelderman, Jim Gerwing, Dwayne Winther, and Brian Pavel (South Dakota State University); and L. Hesler, W. Riedell, and S. Osborne (USDA-ARS-NGIRL).

***Personnel changes.***

Dr. Jeff Stein joined the faculty of the Plant Science Department as the small grains pathologist and assistant professor of plant science in September 2004. He received his B.S. degree in botany and plant pathology (1997) and Ph.D. degree in plant pathology (2002) from Michigan State University in East Lansing. He was a postdoctoral research associate at the Texas Agricultural Experiment Station in Bushland from 2002–04 where he conducted research on the survival and QPCR-based quantification of *T. indica* teliospores in soil. Dr. Stein directs a research program that focuses on the fungal diseases of small grains. His current research interests include the epidemiology of *Fusarium* head blight, common root rot, and tan spot. Dr. Stein is also an instructor for two courses in plant pathology at SDSU.

***Winter wheat breeding and genetics.***

A.M.H. Ibrahim, S.A. Kalsbeck, R.S. Little, and S. Malla.

**Crop report and testing sites.** Winter wheat production in 2004 was estimated at  $56.25 \times 10^6$  bushels, down 9 % from last year. Grain yield averaged 45 bu/acre, which is two bushels above last year and is the second highest in the state's history. Producers harvested  $1.25 \times 10^6$  bushels from 1.65 acres, down 13 % from 2003.

In 2004, the winter wheat breeding program conducted testing at eight sites throughout South Dakota. These environments included Aurora and Brookings (Brookings Co.), Platte (Douglas Co.), Highmore (Hyde Co.), Selby (Walworth Co.), Winner (Tripp Co.), Wall (Pennington Co.), the Northeast Research Farm near Watertown (Codington Co.), Kennebec (Lyman Co.), and both irrigated and dry land environments at the Dakota Lakes Research Farm east of Pierre (Hughes Co.). Crop performance testing also was conducted at an additional nine sites west of the Missouri River in coöperation with John Rickertsen and Bruce Swan (SDSU West River Agricultural Research and Extension Center, Rapid City).

Autumn stand establishment at most testing locations was below average. After a very dry, mild winter, the crop was rated at 58 % poor to very poor by the State Statistics Report. The Kennebec site in Lyman Co. was lost due to high winds that covered the nursery with drifting soil. Dry conditions early in the growing season significantly pushed winter wheat flowering ahead of the 5-year average. However, 6 weeks of cool wet weather in May and June significantly extended the grain-filling duration ahead of the 5-year average in eastern parts of the state, resulting in record yield in some of these areas.

**Research.** Our research continues to focus on line development, characterization, and applied studies in areas with potential to contribute to cultivar release. Crossing and germ plasm-enhancement efforts continue to address high yield potential, end-use quality, and important biotic and abiotic constraints facing producers in South Dakota and the Northern Great Plains.

Basic research support projects include end-use quality enhancements and inheritance studies on resistance to FHB, stem rust, and freeze survival.

In 2004, we screened 1,498 genotypes in a FHB mist-irrigated field nursery. The percentage of the South Dakota experimental lines that were superior to the FHB resistant check Expedition (disease index (incidence % \* severity%/100) = 16.8 %) was 14.6 %. Advanced lines also were evaluated in the greenhouse using needle inoculation and were screened for the 3BS QTL associated with the Sumai 3-type resistance. Six genotypes, consisting of susceptible winter wheat Nekota and 2137, moderately susceptible winter wheat Harding, moderately resistant spring wheats ND2710 and BacUp, and resistant spring wheat Ning7840, were crossed in a partial diallel mating design to determine combining ability of FHB resistance. F<sub>1</sub> crosses were evaluated in the greenhouse, and F<sub>2</sub> crosses were screened under both greenhouse and mist-irrigated field conditions. One parent, Nekota, was excluded from the diallel mating design in the field condition because of few F<sub>2</sub> seed and poor plant stand. In the greenhouse, both F<sub>1</sub> and F<sub>2</sub> were artificially point inoculated at anthesis, whereas F<sub>2</sub> crosses in field conditions were artificially inoculated by a combination of corn-spawn spread at jointing stage and inoculum-suspension spray at anthesis. Disease index percentage of the crosses was analyzed using Griffing's method 4 and model 1. General combining ability was highly significant ( $P < 0.01$ ) in both greenhouse and field conditions, but specific combining ability was significant ( $P < 0.05$ ) only in F<sub>2</sub> crosses grown in the greenhouse. The results showed that both additive and nonadditive gene effects are involved in the inheritance of FHB resistance.

We crossed several novel/under-utilized, broad-spectrum, stem rust-resistance genes into selected adapted lines. The F<sub>2</sub> seed were planted in the greenhouse in February 2005. Our objective is to search for molecular markers linked to some of these genes in collaboration with Dr. Yang Yen, SDSU Molecular Microbiologist, and Dr. Jeff Stein, small grains pathologist.

**New release. Wendy**, the first HWWW from South Dakota, was released to seed producers for planting in 2004. Wendy is an early maturing line that combines good noodle quality, excellent winter survival, and high yield potential.

**Foundation seed increase.** One line (SD97W609) is being increased for Foundation Seed with potential release in 2006. SD97W609 was developed from the cross 'Abilene/Karl' and is a semidwarf, early-maturing (similar to Wendy) HWWW with good winter survival ability and excellent yield potential. Wendy has excellent baking quality in predictive testing and in large-scale testing in the 2005 Wheat Quality Council. The cultivar has a high test weight, intermediate levels of polyphenoloxidase enzyme, average protein, very short coleoptile, and good sprouting resistance. Wendy is moderately resistant to stem rust and WSMV and is moderately susceptible to leaf rust.

### *Cereal aphids.*

L. Hesler, W. Riedell, and S. Osborne (USDA-ARS-NGIRL, Brookings).

In collaboration with scientists at the USDA-ARS research laboratory in Stillwater and at Oklahoma State University, the performance and impact of rice root aphids, *Rhopalosiphum rufiabdominalis*, on various cereal and grass hosts was determined. Rice root aphids infest small grains throughout North America. For instance, we examined winter wheat fields in central South Dakota that were heavily infested with cereal aphids in the autumn of 1997 and 1999, and rice root aphids were the predominant aphids in these fields. However, little is known about their alternate hosts, appropriate techniques for rearing rice root aphids or their impact on cereal production. Rice root aphids were obtained by collecting numerous individuals from a winter wheat field near Brookings, SD, in autumn 1999. A low-cost technique for large-scale rearing of rice root aphid was developed using a soil-based medium with cedar chips used to cover seeds of the host plant (Elbon rye). This approach, which requires minimal labor and no specialized equipment, was used to establish colonies at facilities in Brookings and Stillwater. Rice root aphids were then used in greenhouse tests to evaluate survival and reproduction on selected grasses and cultivated cereals. Elbon rye and Altai wild rye were determined to be the most suitable hosts from 15 candidates, based on reproductive rates and aphid survival. These cereals were followed by TAM 110 wheat, OK 91806 barley, and Okay oats. Rice and sorghum were poor hosts, and corn was a nonhost. Generally, grasses were inferior hosts for rice root aphids when compared with cultivated cereals.

In a second study with Oklahoma scientists, field abundance of the rice root aphid was studied over a 2-year period in central Oklahoma. Rice root aphid and other aphid species (corn leaf aphid, *R. maidis*; bird cherry-oat aphid, *R. padi*; and greenbug, *S. graminum*) colonized winter wheat in Oklahoma during the autumns of 2001 and 2002. During each of the 2 years, rice root aphids infested winter wheat soon after emergence and continued to increase in number on the autumn-seeded crop until mid December when populations peaked and then began to decline, so that by

early January the aphids were difficult to find. Rice root aphid populations of 3.6 aphids/tiller at the end of a 60-day infestation period reduced forage yield of wheat, which can be a significant economic impact for winter wheat that is grazed by cattle. Grain yield was not significantly reduced. Additional studies are underway to determine the impact of controlled infestations of viruliferous and nonviruliferous rice root aphids on yield loss in wheat.

### **Publications.**

Kindler SD, Hesler LS, Elliott NE, Shufron KS, and Springer TL. 2003. Cereal and grass hosts of the rice root aphid, *Rhopalosiphum rufiabdominalis*, and a description of an efficient greenhouse rearing technique. J Agric Urban Entomol 20:51-59.

Kindler SD, Hesler LS, Elliott NE, Royer T, and Giles K. 2004. Seasonal abundance of rice root aphid in wheat and effects on forage and grain yields. Southwest Entomol 29:245-252.

### **Crop nutrient influences on wheat production.**

Howard J. Woodard, Anthony Bly, Ron Gelderman, Jim Gerwing, Dwayne Winther, and Brian Pavel.

**Nitrogen timing influence on HRSW grain protein and yield.** Soil test nitrate-N (0-24") of 45 lbs/acre in a field near Aurora, SD, determined that 80 lbs/acre N would be required to support a 50 bu/acre yield goal. A lower than recommended N application rate as ammonium nitrate was applied (50 lbs/acre) at planting to avoid over-applying the fertilizer N requirement so that treatment differences could be observed. A control and high N rate (100 lbs/acre) also was applied at planting. Briggs HRSW was no-till planted at 1.2 million pure live seeds/acre. The 50 lbs/acre N application was applied either on 7 April (planting), 7 May (tillering), 3 June (jointing), 9 June (boot), or 23 June (heading). Plots were harvested with a small plot combine on 19 August. Grain protein was measured with near infrared reflectance spectroscopy.

The greatest grain yield was obtained with a rate of 50 lbs/acre N fertilizer applied at planting. Because N was applied later in the growing season, yield was reduced. Grain protein was highest with N treatment representing the lowest grain yield. Typically, the highest yielding wheat has the lowest protein content except when an abundance of N is available. The high N rate (100 lbs N/acre) did not have the lowest grain protein. No grain yield increase was gained from the addition of 50 lbs N/acre resulting in a sufficient amount of N available for protein, which was similar to lower-yielding treatments. As N rate increased from 0 to 50 lbs N/acre, grain increased significantly from 47 and 62 bu/acre, respectively. Increasing the N rate to 100 lbs/acre N rate did not increase the grain yield (62.1 bu/acre). Grain protein increased from 13.3 % to 15.5 % as N timing applications progressed from the planting to the heading stage.

**Influence of liquid and dry nitrogen fertilizer materials on grain protein and yield of HRSW.** Briggs HRSW was seeded in 7-in rows at  $1.2 \times 10^6$  pure live seeds/acre on 7 April in a no-till field near Aurora, SD. Fertilizer N at a rate of 100 lbs N/acre as urea was broadcast applied on all plots after planting, which was recommended for a 50 bu/acre yield goal. Four different N treatments at a rate of 30 lbs N/acre were applied on 7 July at the pollination growth stage (Feekes' stage 10) and dry or liquid ammonium nitrate (AMN) or dry or liquid urea ammonium nitrate (UAN) along with a control (0 lbs N/a). The rate of application for both liquid fertilizer materials was 20 gal/a. The liquid UAN solution was a 1:1 blend with water. Rain was received 4 and 5 days after treatment application (0.75 and 0.88 inches, respectively); adequate time for the foliar treatment applications to be absorbed by plant foliage and enough rain to incorporate the dry fertilizer into the soil for root absorption. Grain was harvest from the plots with a small plot combine on August 19, 2004. Grain protein increased significantly by all treatments when compared to the check from 57- 62 bu/acre. Some orthogonal contrasts for grain yield were significant and indicated that yield was higher for the dry fertilizer materials and severely decreased by the AMN liquid treatment applied at pollination. The orthogonal contrasts for grain protein indicated that all treatments increased grain protein when compared to the control. Dry fertilizer materials performed just as well as liquid in increasing grain protein at the pollination growth stage if there is adequate rainfall following the application. This data would suggest that plant tissue absorbed N from foliar applications of liquid fertilizer material and was not being washed off and taken up by the roots, indicated by the equal performance of both the dry and liquid fertilizer materials in increasing grain protein.

**Managing cultural practices for high spring wheat yields.** A field near Brookings, SD, was chosen to evaluate the impact of five cultural practices on the yield of Briggs HRSW planted on 7 April: soil fertility with a sulfur comparison,

split application of nitrogen, seeding rate, foliar fungicide, and a fungicide seed treatment. The five cultural practices were employed to compare with standard recommended methods for successful wheat production. A comparison of soil fertility was made between standard nutrient recommendations determined from soil test results for a 60 bu/acre yield goal and nutrient applications for 100 bu/acre yield goal. The split application of nitrogen was evaluated by splitting the N for the 100 bu/acre yield goal into three timings; planting, tillering, and boot growth stages. The standard seeding rate of  $1.2 \times 10^6$  pure live seeds (PLS)/acre was compared to  $2.2 \times 10^6$  PLS/acre. Applying 4 oz/acre Tilt at flag leaf and 4 oz/acre Folicur at heading was the treatment used for disease control. The fungicide seed treatment used was Raxil XT (0.16 oz/100 lbs seed). Tilt (4 oz/acre) and Folicur (4 oz/acre) were applied on 9 and 22 June, respectively. Plots were harvested with a small plot combine on 19 August, 2004. Grain protein was determined with standard NIR technique.

Orthogonal contrasts for the soil fertility treatment showed that grain test weight was significantly higher with the recommended treatments over the control and higher fertilizer levels. Grain protein and yield were higher for the maximum treatments. More nutrients were applied to the maximum treatments, so it was difficult to determine which nutrient increased grain yield. However, the influence of nitrogen probably had the greatest impact on grain yield increases, because the grain protein increased above the true check (12.4 %) and above the recommended rate (13.5 %). The true check and recommended treatment plots were nitrogen stressed as indicated by lower grain protein. Seeding rate significantly increased grain test weight and protein over the recommended seedling rate. Applying foliar fungicide increased yield by 7.5 bu/acre over the fungicide control treatment. The seed treatment did not significantly influence any of the dependent variables. The split N application significantly increased grain test weight and protein. A sulfur application (25 lbs/acre) significantly decreased grain protein and yield.

**Crop rotation, tillage, and crop residue management influences on HRWS yields.** Briggs HRSW was seeded at  $1.2 \times 10^6$  pure live seeds in tilled or no-till plots on 7 April. Straw was returned to the residue-maintenance plots and removed from the residue-removal plots on 26 August. Spring wheat and soybean grain proteins and soybean grain oil were measure by standard NIR techniques. Neither tillage, crop rotation, nor residue management influenced grain yield (61–68 bu/acre). However, residue removal increased the grain yield of wheat (71 bu/acre) planted in no-till compared to the residue-maintained plots (59 bu/acre), presumably because of increased temperature of the bare soil during emergence and early season growth.

## VIRGINIA

**VIRGINIA POLYTECHNIC INSTITUTE AND STATE UNIVERSITY**  
**Department of Crop and Soil Environmental Sciences, Blacksburg, VA 24061, U.S.A.**

J.J. Paling, C.A. Griffey, W.E. Thomason, J. Chen, J.A. Wilson, D. Nabati, T.H. Pridgen, M.M. Alley, and E.G. Rucker.

### ***2004 wheat production in the Commonwealth of Virginia.***

J.J. Paling, C.A. Griffey, W.E. Thomason, and M.M. Alley.

**Growing conditions.** Although weather conditions in 2004 were more favorable for wheat planting, growth, and harvest than in 2003, grain yields and test weights were impacted by hot temperatures during the grain-fill period. Autumn temperatures were warm through October and into mid November during the planting season. Temperatures eventually declined and were colder than average and precipitation was slightly below normal for much of the state during the winter. Average daily temperatures through March 2004 were 5 degrees below normal for the entire state. Many small grain fields lacked optimal growth and tillering was poor in the early spring. Late planting, inadequate topsoil moisture, and especially the cold temperatures were contributing factors leading to delayed heading. Warmer, dry weather arrived in late April. The month of May was dry and warmer than normal for much of the eastern part of the state. Temperatures exceeded 85°F (29°C) on 19 days in May at the experiment station near Warsaw, VA. Similar hot and dry conditions were experienced throughout much of eastern Virginia during May, 2004. Despite later than normal heading, wheat

ripened considerably earlier due to the high temperatures. Wheat harvest began ahead of schedule, but was delayed by rain and cloudy weather later in June.

**Insects.** Populations of the cereal leaf beetle and aphids attracted the attention of wheat producers in 2004. High numbers of aphids were found in wheat fields over most of the eastern wheat production area in late April. Scouting was advised to determine whether aphid populations had reached threshold control levels. Control measures were recommended when populations reached threshold and there was little activity of natural enemies in the field. Cereal leaf beetle populations reached economic threshold level later than usual in 2004 and persisted longer than anticipated. Highest populations and damage were reported in late-planted wheat fields having a low amount of foliage and in cover-crop fields. Scouting was recommended through mid May in untreated fields on the eastern shore.

**Disease incidence and severity.** Powdery mildew incidence and severity were lower than usual for the second consecutive year in the Eastern Shore and Coastal Plain regions because of excessive precipitation in 2003 and early and persistent hot May temperatures in 2004. Leaf rust incidence and severity were minimal in most of the wheat production area, but were moderate to severe on susceptible cultivars grown in research trials near Blacksburg. Barley yellow dwarf virus was low to moderate at Warsaw and Blacksburg. The incidence of FHB was much lower in 2004 than in 2003, when epidemics were widespread and severe.

**Production.** The Virginia Agricultural Statistics Service reported in January 2005 that Virginia wheat producers harvested 180,000 acres (72,900 ha) of winter wheat for grain in 2004, representing a 12 % increase over 2003. More than 85 % of the 210,000 acres (85,000 ha) of winter wheat planted was harvested for grain in 2004. Grain yields averaged 55 bu/acre (3,695 kg/ha) in 2004 and were 9 bu/acre (605 kg/ha) higher than the very low 46 bu/acre (3,090 kg/ha) average yield in 2003. Total 2004 wheat production for the Commonwealth was  $9.9 \times 10^6$  bushels (269,380 metric tons).

**State cultivar tests.** A total of 80 entries were evaluated at seven locations across the Commonwealth in 2004. Included in this total were 37 released cultivars and 43 experimental lines (33 developed at Virginia Tech). Three white-seeded lines, one recently released by Virginia Tech, were among the 80 entries in the 2004 tests. Average grain yields ranged from 62 to 78 bu/acre (4,166–5,241 kg/ha) with an overall location and test average of 67 bu/acre (4,502 kg/ha). Wheat cultivars with yields significantly above the test average were USG 3209, SS MPV 57, 99176, USG 3706, SS 8308, USG 3592, and V9412. Seven experimental lines, six from Virginia Tech, also yielded significantly higher than the average. Yields of the highest producing cultivars and experimental lines ranged from 71 to 78 bu/acre (4,770–5,241 kg/ha). Average test weights of wheat lines (based on seven locations across the state) ranged from 54.9 lb/bu (706 kg/m<sup>3</sup>) to 59.3 lb/bu (763 kg/m<sup>3</sup>) with a test average of 57.1 lb/bu (735 kg/m<sup>3</sup>). Out of the 26 entries with test weights significantly higher than the test average, 13 were released cultivars and 13 were experimental lines. Only two cultivars (SS 8308 and V9412) and three experimental lines (two from Virginia) had both grain yields and test weights significantly higher than the test average.

**Virginia no-till test.** All 80 wheat entries in the Virginia State wheat test were also planted no-till into corn stubble at the Eastern Virginia AREC near Warsaw, VA, in October 2003. Yields were 10–15 % lower than early season estimates based on late spring tiller and spike numbers. The combination of late heading and subsequent hot weather resulted in a shorter grain-fill period and earlier maturity and led to low yields and test weights, also observed in conventional-till tests at Warsaw. Grain yields averaged 59 bu/acre (3,964 kg/ha) with an average test weight of 57 lb/bu (733 kg/m<sup>3</sup>). The top-yielding cultivars produced more than 65 bu/acre (4,367 kg/ha) in 2004. Released cultivars yielding higher than the test average were SS MPV 57, SS 560, GA931233E17, 99176, Pioneer 26R15, Featherstone 520, USG 3209, and SS8302.

**Virginia wheat yield contests.** There were 11 entries in the 2004 Virginia wheat yield contests. Seven of the entries were grown no-till, three were conventional till, and one entry was with minimum tillage. All of the contestants planted certified seed treated with a fungicide. No-till yields of the 2004 entries averaged slightly higher (2 bu/acre, 134 kg/ha) in 2004 than in 2003. The highest yield under no-till was obtained by George Floyd III of Northampton County. George produced 100 bu/acre (6,719 kg/ha) of Coker 9835 wheat after soybean. Richard Sanford of Westmoreland County entered two fields. Richard produced 86 bu/acre (5,778 kg/ha) of Tribute in one field and 85 bu/acre (5,711 kg/ha) of SS 520 in another field. Frank Hula of Charles City produced 83 bu/acre (5,577 kg/ha) of Renwood 3260. Juan Whittington of Amelia and Joseph Reamy of Richmond harvested 90 and 81 bu/acre, (6,047 and 5,442 kg/ha), respectively, of Sisson wheat. William Crossman of Westmoreland grew 71 bu/acre (4,770 kg/ha) of Pioneer 26R24. The most

dramatic improvement in yield in 2004 versus 2003 was for entries grown using conventional-till systems. Average yield of entries in 2004 was 30 bu/acre (2,016 kg/ha) or 40 percent higher than in 2003. Theo Haberland of Orange County had the highest yield under conventional-tillage. His field of SS 520 yielded 103 bu/acre (6,921 kg/ha) grown after a previous crop of soybean. In Northumberland County, Clifton Brann produced 93 bu/acre (6,249 kg/ha) and the team of Craig and Dan Brann produced 96 bu/acre (6,450 kg/ha) of Tribute wheat after corn. Ronnie Russell of Middlesex produced 82 bu/acre (5,510 kg/ha) of SS 550, which was the only minimum tillage entry in 2004. Congratulations to all contestants in the Virginia Wheat yield contest for producing excellent wheat yields in 2004.

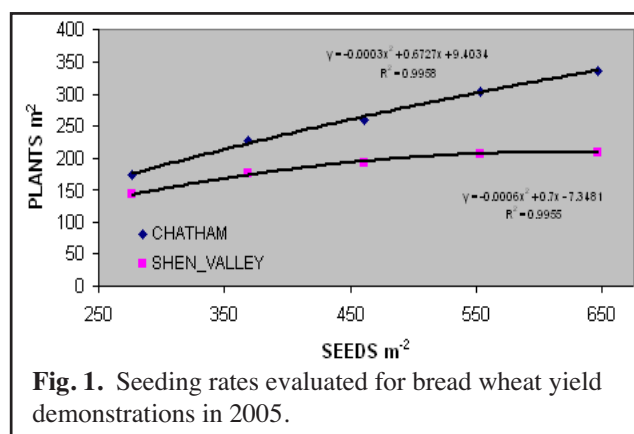
### ***Wheat projects in 2005.***

M.M. Alley, Soil Fertility and Crop Management.

**Research on wheat management.** A survey of the micronutrient content of Virginia wheat is being conducted to determine both the tissue and grain levels associated with major soils used for wheat production. Eight replicated field trials in the 2003–04 growing season found only three responses to micronutrient applications. Two sites produced higher yields with foliar applications of manganese while one site showed a positive response to foliar copper application. All responsive sites were on Coastal Plain soils (sandy texture) with pH values above 6.6. The nonresponsive sites had low levels of dilute acid extractable copper, manganese, and zinc (one field), but pH levels were less than 6.5. These results confirm that micronutrient deficiencies are associated with high soil pH levels and that dilute acid extractable levels of micronutrients are not well associated with crop response. The field trials and the survey of grain micronutrient contents will be repeated in the 2005 growing season.

W.E. Thomason, Small Grain Extension Specialist.

**Research on bread wheat quality.** Promising bread wheat cultivars have been planted in several management trials in the state. These cultivars are being grown with optimal nitrogen management practices. Seeding rate studies have been established in both yield trials and demonstrations. Seeding rates range from below optimum to above optimum (260 to 650 seeds/m<sup>2</sup> or 15 to 35 seeds/row ft) and will be evaluated to determine appropriate seeding rates to optimize yield of bread wheat. Initial plant stands from two locations in the autumn 2004 are presented in Fig. 1.



**Fig. 1.** Seeding rates evaluated for bread wheat yield demonstrations in 2005.

### ***Fusarium head blight resistance incorporated into soft red winter wheat.***

C. A. Griffey, J. Chen, J. A. Wilson, D. Nabati, T. Pridgen, and J. Paling

*Fusarium* head blight is a destructive disease of wheat and barley in the humid and semihumid production areas of the world (Schroeder and Christensen 1963). Scab epidemics have occurred in 26 U.S. states and five Canadian provinces and in the 1990s contributed to yield losses exceeding 500 x 10<sup>6</sup> bushels (Rudd et al. 2001). Monetary losses due to FHB during the past decade have been valued at \$3 billion (Van Sanford et al. 2001). *Fusarium* head blight epidemics in 1998 and 2003 devastated much of the SRWW crop in the mid-Atlantic region. Virginia has been no exception, with epidemic disease levels in 1998 causing losses estimated at 92,595 metric tons, at a value of \$14.4 million (Griffey et al. 1999), reinforcing the need to accelerate development of FHB-resistant cultivars adapted to this region. Specific objectives implemented in the Virginia Tech Breeding Program are to: 1) identify and select FHB-resistant SRWW lines derived from traditional breeding populations; 2) identify and select FHB-resistant wheat lines derived from crosses between nonadapted lines with FHB resistance (type II in particular) and adapted lines possessing resistance to other diseases of economic importance; and 3) accelerate development of FHB-resistant lines using a combination of back-crossing, doubled haploid, and MAS breeding methods.

To develop high yielding, FHB resistant SRW wheat lines, we have deployed a combination of topcross, doubled haploid, backcross, and molecular-marker assisted breeding methods (Tables 1 and 2). We first verified type-II resistance levels in FHB resistance sources currently used in breeding programs. Additionally, we characterized currently cultivated and adapted SRW

wheat genotypes for FHB resistance or susceptibility. We found and confirmed high levels of type-II resistance in six wheat lines from China, three from Canada, one from France, and two from Japan (Chen et al. 2000). We also identified or confirmed the presence of tolerance to kernel infection, yield loss, and DON production in SRWW cultivars, such as Roane, McCormick, and Tribute (Wilson et al. 2003). Initially, we developed a doubled haploid line, VA01W-476, which expressed a high level of resistance in both greenhouse and field trials. This line has been used as a parent in many breeding programs in the eastern United States. We also have made great progress in the development of FHB-resistant lines using top-crossing and backcrossing methods. VA02W-713, a topcross (Ning7840/Pioneer2691//Roane) derived elite FHB-resistant SRWW line, ranked 1st in grain yield (77 bu/acre) among 54 entries in Virginia's 2004 Advance Wheat Test over three locations and will be evaluated in Virginia's Official Variety Trials in 2005.

**Table 1.** Breeding stocks developed and evaluated for FHB resistance by the Virginia Tech breeding program during the past 5 years.

Tests	2001	2002	2003	2004	2005
Segregating Populations	234	147	150	177	100
Headrows	4,000	4,400	7,600	6,500	3,600
Observation Yield Plots	50	61	50	266	359
Preliminary Yield tests	12	12	12	19	64
Advanced, VA-State and Uniform Yield Tests	12	18	14	18	14

**Table 2.** Efficiency of different breeding methods in developing adapted FHB-resistant wheat lines. FHB index < 1.5, incidence < 50 %, number of infected spikelets (severity) < 3.

	Total lines	Resistant no. lines (%)	Best lines no. (%)	Mean yield (bu/acre)	Mean index	Mean incidence (%)	Mean severity
Adapted checks	4	3 (75)		81.6	1.4	49.8	2.8
Top-cross	113	20 (18)	5 (25)	84.8	0.8	38.0	2.2
Doubled-haploid	31	9 (29)	2 (22)	80.8	1.1	37.5	3.0
Backcross	125	35 (28)	19 (54)	86.8	0.9	40.5	2.2

Type-II FHB resistance has been successfully transferred from diverse sources, such as Chinese wheat lines W14, Shaan85, Futai8944, Futai8945, Futai8946, Ning9016, Ning7840, Yumai 7, Er-Mai 9, and Wuhan 1, and the French line VR95B717, into adapted SRWW backgrounds Roane, Ernie, Pioneer 2684, Renwood 3260, Madison, Jackson, and a Sisson sib via backcrossing. Twenty-six SRWW lines possessing both high yield potential and FHB resistance were selected among 268 lines evaluated in Virginia's 2004 Scab Observation tests. These lines will be evaluated in 15 states as part of a collaborative research initiative in 2005. In addition, a set of NILs incorporating FHB resistance QTL from W14 and Futai 8944 into Roane and Ernie backgrounds have been developed using molecular-marker-assisted backcross breeding. Molecular markers in 3BS and 5AS QTL regions are being used to assist in the selection and breeding process. Haplotypes of the 3BS QTL and combinations of haplotypes of 3BS and 5AS QTL are being used to characterize FHB resistance in advanced wheat lines (Table 3, pp. 237-239).

## References.

- Chen J, Griffey CA, Pridgen T, and Chappell M. 2000. Assessment and rational utilization of scab resistance sources in the Virginia Wheat Breeding Program. **In:** Proc Internat Symp on Wheat Improvement for Scab Resistance (Raupp WJ, Ma Z, Chen PD, Liu DJ, Eds). Kansas State University, Manhattan, Kansas. Pp. 10-17.
- Chen J, Griffey CA, Saghai Maroof MA, Stromberg E, Biyashev RM, Zhao W, Chappell M, and Dong Y. 2004. Update on QTL mapping of *Fusarium* head blight resistance in wheat. **In:** Proc 2nd Internat Symp on Fusarium Head Blight, Orlando, FL, 11-15 December, 2004. P. 32.

**Table 3.** Haplotyping of 85 lines on the basis of marker alleles associated with Fusarium head blight resistance identified in W14 (Chen et al. 2004). A plus (+) indicates the presence of marker allele from W14, a minus (–) indicates the absence of marker allele from W14. W14 and VA01W–476 have been confirmed via the capillary method to have a 2-bp difference from other FHB-resistant lines at *Xgwm 533A*. A ‘W’ indicates *Xgwm* primers and ‘B’ indicates *Xbarc* primers.

**KNOWN FHB RESISTANCE SOURCES.**

Line	3BS						5AS				
	B75A	W533A	W533B	W533C	B133B	W493A	B117C	B186A	B56A	B100E	W186E
W14	+	+	+	+	+	+	+	+	+	+	+
Sumai3	+	+	+	+	+	+	+	+	+	–	+
NING7840	+	+	+	+	+	+	+	+	+	–	+
Futai8944	+	+	+	+	+	+	+	+	+	–	+
Frontana	+	+	+	–	–	–	–	+	–	–	–

**NEWLY DEVELOPED SRW WHEAT LINES: REGION.**

Line	3BS						5AS				
	B75A	W533A	W533B	W533C	B133B	W493A	B117C	B186A	B56A	B100E	W186E
Neuse	+	+	+	–	–	–	+	–	+	–	–
Ernie	+	–	–	–	+	–	+	–	+	–	–
TRUMAN	+	+	+	–	–	–	–	–	–	–	–
P99751RA1–6–3	+	+	+	–	–	–	+	+	+	–	+
P97397J1–4–1–4–7	–	–	–	–	+	+	–	–	–	–	–
P97462A1–21–1–5–2	–	+	–	–	+	+	+	+	+	–	–
P981312A1–6–2–2	–	+	+	+	–	–	+	–	+	–	–
P981543A1–1–9–3	+	–	–	–	+	–	–	+	+	–	–
97397J1–4–1–4–7	–	–	–	–	+	+	–	–	–	–	–
AR 857–1–1	–	+	+	–	–	–	–	–	–	–	–
IL97–6755	–	–	–	–	–	–	–	+	+	–	–
IL99–15867	–	+	–	–	–	+	–	–	–	–	–
IL96–24851–1	+	+	–	–	+	+	+	+	+	–	–
COKER B980582	–	–	–	–	–	+	–	–	+	–	–

**NEWLY DEVELOPED SRW WHEAT LINES: VIRGINIA.**

Line	3BS						5AS				
	B75A	W533A	W533B	W533C	B133B	W493A	B117C	B186A	B56A	B100E	W186E
Roane	–	–	–	–	–	+	–	–	–	–	–
Tribute	+	–	–	–	–	–	–	–	–	–	–
McCORMICK	–	–	–	–	–	+	–	–	–	–	–
VA01W–476	+	+	+	+	+	+	+	+	+	+	+
VA02W–713	–	–	–	–	+	+	–	+	+	–	–
VA00W–38	–	–	–	–	–	+	+	–	+	–	–
VA01W–99	–	–	–	–	–	+	–	–	–	–	–

**Table 3 (continued).** Haplotyping of 85 lines on the basis of marker alleles associated with Fusarium head blight resistance identified in W14 (Chen et al. 2004). A plus (+) indicates the presence of marker allele from W14, a minus (–) indicates the absence of marker allele from W14. W14 and VA01W–476 have been confirmed via the capillary method to have a 2-bp difference from other FHB-resistant lines at *Xgwm 533A*. A ‘W’ indicates *Xgwm* primers and ‘B’ indicates *Xbarc* primers.

**BACKCROSS–DERIVED SRW WHEAT LINES: VIRGINIA.**

(RECURRENT PARENT NAMES ARE UNDERSCORED AND PRESENTED ABOVE THEIR RESPECTIVE BACKCROSS DERIVED LINES.)

Line	3BS					5AS					
	B75A	W533A	W533B	W533C	B133B	W493A	B117C	B186A	B56A	B100E	W186E
<u>Jackson</u>	–	+	+	–	–	–	–	–	–	–	–
VA04W–503	–	+	+	–	–	–	–	–	–	–	–
<u>Renwood 3260</u>	–	+	+	–	–	–	–	–	–	–	–
VA04W–513	–	+	+	–	–	–	–	–	–	–	–
VA04W–514	–	+	+	–	–	–	–	–	–	–	–
VA04W–515	–	+	+	–	–	–	–	–	–	–	–
VA04W–517	–	+	+	–	–	–	–	–	–	–	–
<u>Pioneer 2684</u>	–	–	–	–	–	–	–	–	–	–	–
VA04W–520	–	–	–	–	–	–	+	–	+	–	–
VA04W–521	–	+	–	+	–	+	+	–	+	–	–
VA04W–522	–	+	–	+	–	+	–	–	–	–	–
VA04W–535	–	–	–	–	–	–	–	–	–	–	–
VA04W–536	+	+	–	+	+	+	–	–	–	–	–
VA04W–538	–	–	–	–	–	+	–	–	–	–	+
VA04W–547	+	+	–	+	+	+	–	–	–	–	+
VA04W–554	–	–	–	–	–	+	–	–	–	–	–
VA04W–555	–	–	–	–	–	+	–	–	–	–	–
VA04W–557	–	–	–	–	–	+	–	–	–	–	–
VA04W–558	+	+	–	+	–	–	–	–	+	–	–
<u>Roane</u>	–	–	–	–	–	+	–	–	–	–	–
VA03W–644	–	–	–	–	–	+	–	–	–	–	–
VA04W–561	–	–	–	–	–	+	–	–	–	–	–
VA04W–563	+	+	–	+	+	+	–	–	–	–	–
VA04W–568	–	–	–	+	–	+	–	–	–	–	–
VA04W–569	–	–	–	–	–	+	–	–	–	–	–
VA04W–570	–	–	–	–	–	+	–	–	–	–	–
VA04W–571	–	–	–	–	–	+	–	–	–	–	–
<u>Sisson “S”</u>	–	+	+	–	–	–	–	+	+	–	–
VA03W–646	–	+	+	–	–	+	–	+	+	–	–
VA04W–574	–	+	+	–	–	+	–	+	+	–	–
VA04W–575	–	+	+	–	–	+	–	+	+	–	–
<u>Agripro Mason</u>	+	+	+	–	–	+	–	–	–	–	+
VA04W–587	+	+	+	–	+	+	–	–	–	–	+
VA04W–589	+	+	+	–	–	+	–	–	–	–	+
<u>GA891283LE18</u>	–	+	+	–	–	+	–	–	–	–	–
VA04W–592	–	+	+	–	–	+	–	–	–	–	–
<u>Ernie</u>	+	–	–	–	+	–	+	–	+	–	–
VA04W–607	+	–	–	+	+	–	+	–	+	–	–
VA04W–608	+	–	–	–	+	–	+	–	+	–	–
VA04W–611	+	–	–	–	+	–	+	–	+	–	–
VA04W–621	+	–	–	–	+	–	+	–	+	–	–

**Table 3 (continued).** Haplotyping of 85 lines on the basis of marker alleles associated with *Fusarium* head blight resistance identified in W14 (Chen et al. 2004). A plus (+) indicates the presence of marker allele from W14, a minus (–) indicates the absence of marker allele from W14. W14 and VA01W–476 have been confirmed via the capillary method to have a 2-bp difference from other FHB-resistant lines at *Xgwm 533A*. A ‘W’ indicates *Xgwm* primers and ‘B’ indicates *Xbarc* primers.

**BACKCROSS–DERIVED SRW WHEAT LINES: VIRGINIA (CONTINUED).**

Line	3BS						5AS				
	B75A	W533A	W533B	W533C	B133B	W493A	B117C	B186A	B56A	B100E	W186E
VA04W–626	+	–	–	–	+	–	+	–	+	–	–
VA04W–628	+	–	–	–	+	–	+	–	+	–	–
VA04W–629	+	–	–	–	+	–	+	–	+	–	–
VA04W–631	–	–	–	–	–	–	+	–	–	–	–
VA04W–632	+	–	–	–	+	–	+	–	+	–	–

**DOUBLED HAPLOID DERIVED LINES: VIRGINIA.**

Line	3BS						5AS				
	B75A	W533A	W533B	W533C	B133B	W493A	B117C	B186A	B56A	B100E	W186E
VA04W–470	+	+	+	–	+	–	+	+	+	–	–
VA04W–472	–	+	+	–	–	–	–	–	–	–	–
VA04W–474	–	–	–	+	–	+	+	+	+	+	+
VA04W–478	–	–	–	–	–	–	–	–	–	–	–
VA04W–486	+	–	–	–	+	–	–	–	–	–	–
VA04W–491	–	–	–	–	–	+	–	–	–	–	–
VA04W–493	–	–	–	–	–	+	–	–	–	–	+
VA04W–495	–	+	+	–	–	–	–	–	–	–	–
VA04W–498	–	+	+	–	–	–	–	–	–	–	–

**TOPCROSS–DERIVED LINES: VIRGINIA.**

Line	3BS						5AS				
	B75A	W533A	W533B	W533C	B133B	W493A	B117C	B186A	B56A	B100E	W186E
VA04W–360	–	–	–	–	–	+	–	–	–	–	+
VA04W–389	+	–	–	–	+	–	+	–	+	–	–
VA04W–396	–	–	–	+	–	–	–	–	–	–	+
VA04W–404	+	+	+	–	–	–	+	–	+	–	–
VA04W–433	–	–	–	–	+	+	–	+	+	–	–
VA04W–465	–	+	+	+	–	–	–	–	–	–	–

Griffey CA, Chen J, Pridgen T, Chappell M, and Stromberg EL. 1999. Research on *Fusarium* head blight in the Virginia Tech Small Grains Program. **In:** Proc 1999 Eastern & Southern Wheat Workers Conf, 2-4 May, Williamsburg, VA. Pp.95-99. Ann Wheat Newslet 45:281-282.

Rudd JC, Horsley RD, McKendry AL, and Elias EM. 2001. Host plant resistance genes for *Fusarium* head blight: sources, mechanisms, and utility in conventional breeding systems. Crop Sci 41:620-627.

Schroeder HW and Christensen JJ. 1963. Breeding wheat and rye for resistance to *Fusarium* diseases. Phytopath 53:831-838.

Van Sanford D, Anderson J, Campbell K, Costa J, Cregan P, Griffey C, Hayes P, and Ward R. 2001. Discovery and

deployment of molecular markers linked to *Fusarium* head blight resistance: an integrated system for wheat and barley. *Crop Sci* 41:638-644.

Wilson JA, Griffey CA, Chen J, Nabati D, and Pridgen T. 2003. Success of alternative breeding methods in transferring *Fusarium* head blight resistance to soft red winter wheat. **In:** 2003 Natl *Fusarium* Head Blight Forum Proc, 13-15 December, 2003, Bloomington, MN. Pp.295-299.

## **Publications.**

Griffey CA, Rohrer WL, Pridgen TH, Brooks WS, Chen J, Wilson JA, Nabati D, Brann DE, Rucker EG, Behl HD, Vaughn ME, Sisson WL, Randall TR, Corbin RA, Kenner JC, Dunaway DW, Pitman RM, Smid AE, Bockelman HE, Gaines C, Long DL, McVey DV, Cambron SE, and Whitcher L. 2005. Registration of McCormick wheat. *Crop Sci* 45:417-418.

Griffey CA, Rohrer WL, Pridgen TH, Brooks WS, Chen J, Wilson JA, Nabati D, Brann DE, Rucker EG, Behl HD, Vaughn ME, Sisson WL, Randall TR, Corbin RA, Kenner JC, Dunaway DW, Pitman RM, Smid AE, Bockelman HE, Gaines C, Long DL, McVey DV, Cambron SE, and Whitcher L. 2005. Registration of Tribute wheat. *Crop Sci* 45:419-420.

## **WASHINGTON**

### **USDA-ARS, WHEAT GENETICS, QUALITY, PHYSIOLOGY AND DISEASE RESEARCH UNIT, WASHINGTON STATE UNIVERSITY**

**361 Johnson Hall, Washington State University, P. O. Box 646430, Pullman, WA 99164-6430, USA.**

## ***Epidemiology and control of wheat stripe rust in the United States, 2004.***

Xianming Chen, David A. Wood, Laura Penman, and Paul Ling.

**Monitoring rusts, predicting epidemics, assessing yield losses, and identifying races of *Puccinia striiformis* f. sp. *tritici*.** Wheat stripe rust, leaf rust, and stem rust were monitored throughout the Pacific Northwest (PNW) using trap plots and field survey in 2004. The diseases were accurately predicted for the PNW using monitoring data and predictive models based on resistance of wheat cultivars and environmental factors such as temperature and precipitation. Through coöperators in many other states, wheat stripe rust was monitored throughout the United States. In 2004, wheat stripe rust occurred in 17 or more states including Alabama, Arkansas, California, Colorado, Indiana, Kansas, Louisiana, Minnesota, Missouri, Nebraska, Ohio, Oklahoma, Oregon, South Dakota, Texas, Washington, and Wisconsin. Wheat stripe rust was much lighter and its damage was much less in the Great Plains in 2004 than in 2003. However, the disease continued destructive in the Pacific West (California, Oregon, Washington, and Idaho). Stripe rust alerts were sent to growers through E-mails and news releases to implement control with fungicide applications. As a result, most of fields grown with susceptible or moderately susceptible cultivars were appropriately sprayed with fungicides in the PNW. The on-time application of fungicides prevented major losses. The wheat yield losses by stripe rust in Washington State were estimated as 1.5 % for winter wheat and 3 % for spring wheat. A total yield loss of 11,756,000 bushels of wheat by stripe rust in the United States was estimated in 2004 (<http://www.cdl.umn.edu>). In the PNW, leaf rust occurred in some areas but the severity levels were low except in northwestern Washington. Stem rust was not observed.

The epidemic impact of wheat stripe rust and benefit of fungicide control were assessed based on our experimental data and disease survey. In 2004, we evaluated yield reduction by stripe rust and yield increase by fungicide application with 24 winter wheat and 16 spring wheat cultivars in field experiments of randomized split-block design with four replications. Yield losses caused by stripe rust were up to 44 % on susceptible winter wheat and up to 49 % on susceptible spring wheat. Fungicide spray increased yield up to 42 bu/acre for susceptible winter wheat cultivars such as Hatton and 12 bu/acre for susceptible spring wheat cultivars such as Zak. Yield differences between the sprayed and

unsprayed plots were not statistically significant for resistant and moderately resistant cultivars, showing effectiveness of stripe rust resistance, especially high-temperature, adult-plant (HTAP) resistance, in major cultivars in the PNW.

In 2004, 278 wheat stripe rust samples were obtained from 17 states. These samples were evaluated for the virulence/avirulence patterns on 20 wheat genotypes that are used to differentiate races of *P. striiformis* f. sp. *tritici*. Of 32 races detected from these samples, nine (5 % of the samples) were races first identified before 2000. Each of these old races had a frequency less than 1 %. Fourteen races (85 % of the samples) were those first detected from 2000 to 2003. Nine races (10 % of the samples) were first identified in 2004. Each of the new races had a frequency less than 3 %. One of the new races had virulence only on Chinese 166 (*Yr1*), Stephens (*Yr3a*, *YrSte* and *YrSte2*), and AVS-Yr8 (*Yr8*). This race (named PST-110) is the second race avirulent on Lemhi (*Yr21*). All other new races are new variants of the race group exemplified by PST-78 (first identified in 2000; virulent on Lemhi, Heines VII, Lee, Fielder, Express, AVS-Yr8, AVS-Yr9, Clement, and Compair) and PST-100 (first identified in 2003; virulent on Lemhi, Heines VII, Produra, Yamhill, Stephens, Lee, Fielder, Express, AVS-Yr8, AVS-Yr9, Clement, and Compair). Some of the new races have the virulences of PST-100 plus virulences on Moro (*Yr10* and *YrMor*), Paha (*YrPa1*, *YrPa2*, and *YrPa3*), Tres (*YrTr1* and *YrTr2*), and/or Hyak (*Yr17*). PST-100 was the most predominant race throughout the U.S. Genes *Yr5* and *Yr15*, which confer all-stage (often called seedling) resistance, were still resistant to all the races. HTAP resistance, which is nonrace specific and in wheat cultivars like Madsen, Stephens, Daws, Rod, Druchamp, Nugaines, Jagger, and the AVS-Yr18 single gene line, is still effective.

**Test wheat germ plasm and breeding lines for rust resistance.** In 2004, more than 13,000 entries of wheat germ plasm and breeding lines from the National Germplasm Collection Center, various regional nurseries, and public and private wheat breeders in the United States were evaluated for stripe rust resistance in fields under natural infections and in the greenhouse with selected races to cover all possible virulences. All nurseries were evaluated for resistance in both Pullman and Mt. Vernon, WA, and some of the nurseries were also evaluated in Walla Walla and Lind, WA. The germ plasm nurseries and some entries of the regional and breeding nurseries also were evaluated in the greenhouse for resistant to selected races and for HTAP resistance. The wheat entries also were evaluated for resistance to leaf rust, powdery mildew, and physiological leaf spot in field sites when these biotic and abiotic diseases occurred. Disease data of regional nurseries were provided to all breeding and extension programs in that region, whereas data of individual breeders nurseries were provided to the individual breeding programs. Through the germ plasm screening, new cultivars with adequate resistance were released and resistant germ plasm was selected to establish a collection for stripe rust resistance. The current collection has more than 4,000 entries, which should be valuable sources of stripe rust resistance for further characterization of resistance and for development of wheat cultivars with superior resistance.

#### **Determining genetics of resistance, developing molecular markers, and cloning genes for resistance to stripe rust.**

Most wheat genotypes are resistant to barley stripe rust (*P. striiformis* f. sp. *hordei*, PSH) and most barley cultivars are resistant to wheat stripe rust (PST). The wheat genotype Lemhi, which is susceptible to most PST races, is resistant to all tested PSH races. Similarly, the barley cultivar Steptoe, which is susceptible to all PSH races, is resistant to all tested PST races. To determine genetics of the Lemhi resistance to PSH and the Steptoe resistance to PST, crosses were made between Lemhi and PI 478214, a wheat genotype susceptible to all tested PST and PSH races, and between Steptoe and Rusell, a barley cultivar susceptible to some PST races and all tested PSH races. Seedlings of parents and  $F_1$ ,  $BC_1$ ,  $F_2$ , and  $F_3$  progeny from the wheat cross were tested with races PSH-14, PSH-48, and PST-21, and those from the barley cross were tested with races PST-41 and PST-45 under controlled greenhouse conditions. Genetic analyses of infection type data showed that Lemhi had a dominant gene (provisionally designated as *RpsLem*) for resistance to the PSH races and the gene was closely linked to *Yr21*, a previously reported gene for resistance to PST-21; and that Steptoe had a dominant gene and a recessive gene (provisionally designated as *RpstS1* and *rpstS2*, respectively) for resistance to PST-41 and PST-45. For each of the crosses, genomic DNA was extracted from the parents and 150  $F_2$  plants that were tested for rust reaction and production of the  $F_3$  progeny that were tested with the races to confirm the phenotypes and determine genotypes of the  $F_2$  plants. The phenotypic data and polymorphic markers identified using the resistance gene analog polymorphism (RGAP) technique were analyzed with the Mapmaker computer program to map the resistance genes. A linkage group for the genes in Lemhi was constructed with 11 RGAP markers and a linkage group for the dominant gene in Steptoe for resistance to PST races was constructed with 12 RGAP markers. Using an RGAP marker that was linked to the resistant alleles in repulsion and the set of nulli-tetrasomic Chinese Spring lines, the linkage group for *RpsLem* and *Yr21* was mapped on wheat chromosome 1B, which confirmed that chromosomal location of *Yr21*. The dominant gene in Steptoe for resistance to PST races was mapped on barley chromosome 4H using a microsatellite marker HVM68. These genes may provide effective resistance against appropriate pathogens when introgressed into appropriate hosts from inappropriate hosts.

To identify genes for HTAP, as well as for all-stage, resistance and develop molecular markers for the resistance genes, we made crosses among Alpowa, Express, IDO377s, Zak, and Avocet Susceptible (AVS). In 2004,  $F_3$  progeny and parents of the crosses were phenotyped for resistance to stripe rust. Seed of  $F_4$  were harvested and the generations were advanced to  $F_5$ . The mapping populations will be evaluated in multiple field locations for determining the genetics of resistance, identifying genes and developing molecular markers.

Through collaborating with other wheat geneticists and breeders, markers of *Yr5* and *Yr15* were used to combine these genes and incorporate the genes into wheat cultivars. Genes for HTAP resistance were identified from winter wheat 'IDO444' and from *T. turgidum* subsp. *dicoccoides*. Molecular markers were identified for QTL on chromosome 6B controlling HTAP resistance in Stephens.

To clone stripe rust resistance genes, a BAC library for hexaploid wheat was constructed. The BAC library consists of 410,000 clones with an average insert size of 130 kb, and covers approximately 3.3X wheat genome equivalents. Using the BAC library, 12 positive BAC clones containing molecular markers for *Yr5* were identified. A full-length cDNA library consisting of 42,000 clones with an average cDNA length of 1.5 kb also was constructed to facilitate the *Yr* gene cloning.

**Determining the effectiveness and use of foliar fungicides for rust control.** Fungicides were evaluated for controlling stripe rust in experimental fields near Pullman, WA. Susceptible winter wheat cultivars Hatton and PS 279 were planted on 22 October, 2003, and spring wheat Lemhi was planted on 22 April, 2004, using a completely randomized block design with four replications. Six treatments with four fungicides (Quilt, Tilt, Stratego, and Headline) were tested with nontreatments as checks. Fungicides were sprayed on 6 June in the winter plots when the plants were at the boot stage with 1 % stripe rust and on 19 June in the spring plots when the plants also were at the boot stage with 10 % stripe rust. A second spray was only used for one of the treatments with Quilt. Severities of stripe rust were recorded three times after fungicide application. Test weight and yield were recorded for each plot at the time of harvesting. All of the fungicide treatments effectively reduced stripe rust severity. Stripe rust started redeveloping about 1 month after the application and therefore the fungicides kept effective for about 1 month. The treatments increased yield by 30–50 bu/acre (46–67 %) for PS 279, 36–42 bu/acre (50–58 %) for Hatton, and 7–18 (18–48 %) for Lemhi. The two-applications of Quilt best controlled stripe rust, but did not significantly increase yield compared to the one-application of Quilt and some other fungicides.

### *Manganese superoxide dismutase.*

Daniel Z. Skinner, Kwang-Hyun Baek and Brian S. Bellinger.

A BAC constructed from hexaploid wheat and containing a gene encoding manganese superoxide dismutase was identified. The region containing the gene was sequenced. The gene consisted of five introns and six exons, similar to MnSOD genes from other plants and animals. The promoter region contained several stress- and hormone-responsive elements, suggesting wheat MnSOD is directly responsive to environmental conditions and is subject to hormonal regulation.

### *Evaluation of phospholipid acyl chain composition changes during cold acclimation of wheat.*

Daniel Z. Skinner, Kwang-Hyun Baek and Brian S. Bellinger.

That wheat accumulates additional phospholipid in the cell membranes in response to exposure to cold temperatures is well known. We investigated the dynamics of the structural composition of the acyl side chains during a 5-week exposure of five winter wheat cultivars to vernalizing temperatures. The proportion of phospholipids with mismatched acyl chains decreased concomitantly with an increase in total phospholipids during the first week of cold exposure. Proportions of mismatched acyl chains then increased, while total phospholipid content varied little. Newly-synthesized phospholipids with equal-length acyl chains appear to form a part of the initial response to cold temperature; they are then modified to contain near-initial levels of mismatched acyl chains during acclimation.

**Long oligonucleotide microarrays from wheat.**

Daniel Z. Skinner, Kwang-Hyun Baek and Brian S. Bellinger.

Microarrays were printed with 95 oligonucleotides (60 mers) representing 41 wheat genes. The microarray was interrogated with cDNA from hexaploid wheat roots and shoots from a near-isogenic lines (NIL) pair differing at the *vrn1-Fr1* locus, and a commercial cultivar. The wheat lines were challenged with cold temperature, hot temperature, or the biological control bacterium *Pseudomonas fluorescens*. Self-complementarity of the oligonucleotides was negatively correlated with signal intensity in 23 of 54 arrays (39%;  $P < 0.01$ ). Tyramide signal amplification was essential for signal generation and detection. Genes involved in signal transduction pathways responded similarly following exposure to cold, heat and *P. fluorescens*, suggesting intersection of the pathways involved in response to these disparate stress factors.

**Publications.**

- Akkaya MS, Chen XM, Bozkurt O, Yildirim F, Unver T, and Somel M. 2004. Isolation of RGAs and disease related gene fragments from wheat stripe rust resistant differential lines. **In:** Proc 11th Internat Cereal Rusts and Powdery Mildews Conf, Norwich, England, 22-27 August, 2004. Abstract A2.1, Cereal Rusts and Powdery Mildews Bull.
- Chen XM. 2004. Stripe rust epidemiology and control in the United States. **In:** Abstr 15th Internat Plant Protection Cong, 11-16 May 2004, Beijing, China. P. 351.
- Chen XM and Ling P. 2004. Towards cloning wheat genes for resistance to stripe rust and functional genomics of *Puccinia striiformis* f. sp. *tritici*. **In:** Proc 11th Internat Cereal Rusts and Powdery Mildews Conf, Norwich, England, 22-27 August, 2004. Abstract A2.10, Cereal Rusts and Powdery Mildews Bull.
- Chen XM, Ling P, Wood DA, Moore MK, and Pahalawatta V. 2004. Epidemiology and control of wheat stripe rust in the United States, 2003. *Ann Wheat Newslet* 50:274-277.
- Chen XM, Milus EA, Long DL, and Jackson LF. 2004. Impact of wheat stripe rust and races of *Puccinia striiformis* f. sp. *tritici* in the United States. **In:** Proc 11th Internat Cereal Rusts and Powdery Mildews Conf, Norwich, England, 22-27 August, 2004. Abstract A2.11, Cereal Rusts and Powdery Mildews Bull.
- Chen XM, Moore MK, and Wood DA 2004. Stripe rust epidemics and races of *Puccinia striiformis* in the United States in 2003. *Phytopath* 94:S18.
- Chen XM and Pahalawatta V. 2004. Genetics and molecular mapping of resistance genes in wheat and barley against inappropriate formae speciales of *Puccinia striiformis*. **In:** Proc 11th Internat Cereal Rusts and Powdery Mildews Conf, Norwich, England, 22-27 August, 2004. Abstract A2.9, Cereal Rusts and Powdery Mildews Bull.
- Chen XM and Wood DA. 2004. Control of stripe rust of spring wheat with foliar fungicides, 2003. *Fung and Nemat Tests* 59:CF022.
- Chen XM, Yan GP, Soria MA, Dubcovsky J, and Hayes PM. 2004. RGAP, STS, and CAPS markers for disease resistance genes in wheat and barley. **In:** Abstr 15th Internat Plant Protection Cong, 11-16 May 2004, Beijing, China. P. 263.
- Kidwell KK, DeMacon VL, Shelton GB, Burns JW, Carter BP, Morris CF, and Chen XM. 2004. Registration of 'Eden' wheat. *Crop Sci* 44:1870-1871.
- Kidwell KK, Shelton GB, DeMacon VL, Burns JW, Carter BP, Morris CF, Chen XM, and Bosque-Perez NA. 2004. Registration of 'Hollis' wheat. *Crop Sci* 44:1871-1872.
- Li HJ, Conner RL, McCallum BD, Chen XM, Su H, Wen ZY, Chen Q, and Jia X. 2004. Resistance of Tangmai 4 wheat to powdery mildew, stem rust, leaf rust, and stripe rust and its chromosome composition. *Can J Plant Sci* 84:1015-1023.
- Ling P, Du WW, Le DQ, and Chen XM. 2004. Construction of a hexaploid wheat (*Triticum aestivum* L.) BAC library for cloning genes conferring resistance to stripe rust. *Plant and Animal Genome XII*. P. 144.
- Markell SG, Milus EA, and Chen XM. 2004. Genetic diversity of *Puccinia striiformis* f. sp. *tritici* in the United States. **In:** Proc 11th Internat Cereal Rusts and Powdery Mildews Conf, Norwich, England, 22-27 August, 2004. Abstract A2.23, Cereal Rusts and Powdery Mildews Bull.
- Pahalawatta V and Chen XM. 2004. Inheritance of and molecular mapping of wheat and barley genes for resistance to inappropriate formae speciales of *Puccinia striiformis*. *Phytopath* 94:S80.
- Wan AM, Zhao ZH, Chen XM, He ZH, Jin SL, Jia QZ, Yao G, Yang JX, Wang BT, Li GB, Bi YQ, and Yuan ZY. 2004. Wheat stripe rust epidemics and virulence of *Puccinia striiformis* f. sp. *tritici* in China in 2002. *Plant Dis* 84:1015-1023.

- Skinner DZ, Bellinger BS, Halls S, Baek K-H, Garland-Campbell K, and Siems WF. 2005. Phospholipid acyl chain and phospholipase dynamics during cold acclimation of winter wheat. *Crop Sci* (In press).
- Skinner DZ, Okubara PA, Baek K-H, and Call DR. 2005. Long oligonucleotide microarrays in wheat: evaluation of hybridization signal amplification and an oligonucleotide-design computer script. *Funct Integrat Genomics* (In press).